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OM protein - protein search, using sw model

Run on: November 12, 2003, 11:07:32 ; Search time 21 Seconds
(without alignments)
62.459 Million cell updates/sec

Title: US-09-446-543A-5
Perfect score: 172
Sequence: 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	172	100.0	31	3	US-09-105-678A-7	Sequence 7, Appli
2	172	100.0	31	3	US-09-105-678A-31	Sequence 31, Appl
3	172	100.0	31	3	US-08-776-971-5	Sequence 5, Appli
4	172	100.0	31	3	US-08-776-971-97	Sequence 97, Appl
5	172	100.0	31	3	US-09-421-208-7	Sequence 7, Appli
6	172	100.0	31	3	US-09-421-208-31	Sequence 31, Appl
7	172	100.0	31	4	US-09-560-915-13	Sequence 13, Appl
8	172	100.0	32	3	US-09-105-678A-32	Sequence 32, Appl
9	172	100.0	32	3	US-08-776-971-6	Sequence 6, Appli
10	172	100.0	32	3	US-09-421-208-32	Sequence 32, Appl
11	172	100.0	33	3	US-09-105-678A-33	Sequence 33, Appl
12	172	100.0	33	3	US-08-776-971-7	Sequence 7, Appli
13	172	100.0	33	3	US-09-421-208-33	Sequence 33, Appl
14	172	100.0	98	3	US-08-776-971-1	Sequence 1, Appli
15	172	100.0	98	3	US-08-776-971-44	Sequence 44, Appl
16	172	100.0	98	3	US-08-776-971-122	Sequence 122, App
17	172	100.0	98	3	US-08-776-971-131	Sequence 131, App
18	172	100.0	98	3	US-08-776-971-136	Sequence 136, App
19	168	97.7	98	3	US-08-776-971-115	Sequence 115, App
20	168	97.7	98	3	US-08-776-971-117	Sequence 117, App
21	163	94.8	31	3	US-09-105-678A-8	Sequence 8, Appli
22	163	94.8	31	3	US-09-105-678A-37	Sequence 37, Appl
23	163	94.8	31	3	US-09-172-353-4	Sequence 4, Appli
24	163	94.8	31	3	US-08-776-971-47	Sequence 47, Appl
25	163	94.8	31	3	US-09-421-208-8	Sequence 8, Appli
26	163	94.8	31	3	US-09-421-208-37	Sequence 37, Appl
27	163	94.8	31	4	US-09-560-915-14	Sequence 14, Appl
28	163	94.8	31	4	US-09-799-955-4	Sequence 4, Appli
29	163	94.8	32	3	US-09-105-678A-38	Sequence 38, Appl
30	163	94.8	32	3	US-08-776-971-48	Sequence 48, Appl
31	163	94.8	32	3	US-09-421-208-38	Sequence 38, Appl
32	163	94.8	33	3	US-09-105-678A-39	Sequence 39, Appl
33	163	94.8	33	3	US-08-776-971-49	Sequence 49, Appl
34	163	94.8	33	3	US-09-421-208-39	Sequence 39, Appl
35	163	94.8	83	3	US-08-776-971-45	Sequence 45, Appl
36	163	94.8	83	3	US-08-776-971-124	Sequence 124, App
37	163	94.8	83	3	US-08-776-971-137	Sequence 137, App
38	161	93.6	29	3	US-09-105-678A-29	Sequence 29, Appl
39	161	93.6	29	3	US-08-776-971-3	Sequence 3, Appli
40	161	93.6	29	3	US-09-421-208-29	Sequence 29, Appl
41	158	91.9	31	3	US-09-105-678A-9	Sequence 9, Appli
42	158	91.9	31	3	US-09-105-678A-43	Sequence 43, Appl
43	158	91.9	31	3	US-08-776-971-61	Sequence 61, Appl
44	158	91.9	31	3	US-09-421-208-9	Sequence 9, Appli
45	158	91.9	31	3	US-09-421-208-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-09-105-678A-7
; Sequence 7, Application US/09105678A
; Patent No. 6103882
; GENERAL INFORMATION:
; APPLICANT: Suenaga, Masato
; APPLICANT: Moriya, Takeo
; APPLICANT: Tanaka, Yoko
; APPLICANT: Nishimura, Osamu
; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,678A
; FILING DATE: 26-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 172118/1997
; FILING DATE: 27-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Conlin, David G.
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 48466-342
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-105-678A-7

Query Match 100.0%; Score 172; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

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                    ||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 2
US-09-105-678A-31
; Sequence 31, Application US/09105678A
; Patent No. 6103882
;  GENERAL INFORMATION:
;    APPLICANT:  Suenaga, Masato
;    APPLICANT:  Moriya, Takeo
;    APPLICANT:  Tanaka, Yoko
;    APPLICANT:  Nishimura, Osamu
;    TITLE OF INVENTION:  METHOD OF PRODUCING A 19P2 LIGAND
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/105,678A
;      FILING DATE:  26-JUN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 172118/1997
;      FILING DATE:  27-JUN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Conlin, David G.
;      REGISTRATION NUMBER:  27,026
;      REFERENCE/DOCKET NUMBER:  48466-342
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-105-678A-31

  Query Match             100.0%;  Score 172;  DB 3;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-19;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              ||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 3
US-08-776-971-5
; Sequence 5, Application US/08776971B
; Patent No. 6228984
;   GENERAL INFORMATION:
;        APPLICANT: Hinuma, Shuji
;                   Habata, Yugo
;                   Kawamata, Yuji
;                   Hosoya, Masaki
;                   Fujii, Ryo
;                   Fukusumi, Shoji
;                   Kitada, Chieko
;        TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
;        NUMBER OF SEQUENCES: 140
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;             STREET: 130 Water Street
;             CITY: Boston
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/776,971B
;             FILING DATE: 06-Feb-1997
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/JP96/03821
;             FILING DATE: 28-DEC-1996
;             APPLICATION NUMBER: JP 7/343371
;             FILING DATE: 28-DEC-1995
;             APPLICATION NUMBER: JP 8/59419
;             FILING DATE: 15-MAR-1996
;             APPLICATION NUMBER: JP 8/211805
;             FILING DATE: 12-AUG-1996
;             APPLICATION NUMBER: JP 8/246573
;             FILING DATE: 18-SEP-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Conlin, David G.
;             REGISTRATION NUMBER: 27,026
;             REFERENCE/DOCKET NUMBER: 47176
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 617-523-3400
;             TELEFAX: 617-523-6440
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 31 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        FRAGMENT TYPE: internal
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-08-776-971-5

  Query Match             100.0%;  Score 172;  DB 3;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-19;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              ||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 4
US-08-776-971-97
; Sequence 97, Application US/08776971B
; Patent No. 6228984
;   GENERAL INFORMATION:
;        APPLICANT: Hinuma, Shuji
;                   Habata, Yugo
;                   Kawamata, Yuji
;                   Hosoya, Masaki
;                   Fujii, Ryo
;                   Fukusumi, Shoji
;                   Kitada, Chieko
;        TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
;        NUMBER OF SEQUENCES: 140
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;             STREET: 130 Water Street
;             CITY: Boston
;             STATE: MA
;             COUNTRY: USA
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; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,971B
; FILING DATE: 06-Feb-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/03821
; FILING DATE: 28-DEC-1996
; APPLICATION NUMBER: JP 7/343371
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: JP 8/59419
; FILING DATE: 15-MAR-1996
; APPLICATION NUMBER: JP 8/211805
; FILING DATE: 12-AUG-1996
; APPLICATION NUMBER: JP 8/246573
; FILING DATE: 18-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Conlin, David G.
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 47176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-08-776-971-97

Query Match 100.0%; Score 172; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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Db 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 5
US-09-421-208-7
; Sequence 7, Application US/09421208
; Patent No. 6258561
; GENERAL INFORMATION:
; APPLICANT: Suenaga, Masato
; APPLICANT: Moriya, Takeo
; APPLICANT: Tanaka, Yoko
; APPLICANT: Nishimura, Osamu
; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/421,208
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/105,678
; FILING DATE: 26-JUN-1998
; APPLICATION NUMBER: JP 172118/1997
; FILING DATE: 27-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Conlin, David G.
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 48466-342
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-421-208-7

Query Match 100.0%; Score 172; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
||||||||||||||||||||||||||||||
Db 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 6
US-09-421-208-31
; Sequence 31, Application US/09421208
; Patent No. 6258561
; GENERAL INFORMATION:
; APPLICANT: Suenaga, Masato
; APPLICANT: Moriya, Takeo
; APPLICANT: Tanaka, Yoko
; APPLICANT: Nishimura, Osamu
; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/421,208
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/105,678
; FILING DATE: 26-JUN-1998
; APPLICATION NUMBER: JP 172118/1997
; FILING DATE: 27-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Conlin, David G.
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 48466-342
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear

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;    MOLECULE TYPE:  peptide
US-09-421-208-31

  Query Match             100.0%;  Score 172;  DB 3;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-19;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 7
US-09-560-915-13
; Sequence 13, Application US/09560915
; Patent No. 6383764
; GENERAL INFORMATION:
;  APPLICANT: Civelli, Olivier
;  APPLICANT:  Lin, Steven
;  TITLE OF INVENTION: Therapeutic Compositions and Methods
;  TITLE OF INVENTION:  Relating To Prolactin Releasing Peptide (PrRP)
;  FILE REFERENCE: P-UC 3534
;  CURRENT APPLICATION NUMBER: US/09/560,915
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Bos taurus
US-09-560-915-13

  Query Match             100.0%;  Score 172;  DB 4;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-19;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 8
US-09-105-678A-32
; Sequence 32, Application US/09105678A
; Patent No. 6103882
;  GENERAL INFORMATION:
;    APPLICANT:  Suenaga, Masato
;    APPLICANT:  Moriya, Takeo
;    APPLICANT:  Tanaka, Yoko
;    APPLICANT:  Nishimura, Osamu
;    TITLE OF INVENTION:  METHOD OF PRODUCING A 19P2 LIGAND
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/105,678A
;      FILING DATE:  26-JUN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 172118/1997
;      FILING DATE:  27-JUN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Conlin, David G.
;      REGISTRATION NUMBER:  27,026
;      REFERENCE/DOCKET NUMBER:  48466-342
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-105-678A-32

  Query Match             100.0%;  Score 172;  DB 3;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-19;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 9
US-08-776-971-6
; Sequence 6, Application US/08776971B
; Patent No. 6228984
;  GENERAL INFORMATION:
;       APPLICANT: Hinuma, Shuji
;                  Habata, Yugo
;                  Kawamata, Yuji
;                  Hosoya, Masaki
;                  Fujii, Ryo
;                  Fukusumi, Shoji
;                  Kitada, Chieko
;       TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
;       NUMBER OF SEQUENCES: 140
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;            STREET: 130 Water Street
;            CITY: Boston
;            STATE: MA
;            COUNTRY: USA
;            ZIP: 02109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/776,971B
;            FILING DATE: 06-Feb-1997
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: PCT/JP96/03821
;            FILING DATE: 28-DEC-1996
;            APPLICATION NUMBER: JP 7/343371
;            FILING DATE: 28-DEC-1995
;            APPLICATION NUMBER: JP 8/59419
;            FILING DATE: 15-MAR-1996
;            APPLICATION NUMBER: JP 8/211805
;            FILING DATE: 12-AUG-1996
;            APPLICATION NUMBER: JP 8/246573
;            FILING DATE: 18-SEP-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Conlin, David G.
;            REGISTRATION NUMBER: 27,026
;            REFERENCE/DOCKET NUMBER: 47176
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 617-523-3400
;            TELEFAX: 617-523-6440
;  INFORMATION FOR SEQ ID NO: 6:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 32 amino acids
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;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        FRAGMENT TYPE: internal
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-776-971-6

  Query Match             100.0%;  Score 172;  DB 3;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-19;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 10
US-09-421-208-32
; Sequence 32, Application US/09421208
; Patent No. 6258561
;  GENERAL INFORMATION:
;    APPLICANT:  Suenaga, Masato
;    APPLICANT:  Moriya, Takeo
;    APPLICANT:  Tanaka, Yoko
;    APPLICANT:  Nishimura, Osamu
;    TITLE OF INVENTION:  METHOD OF PRODUCING A 19P2 LIGAND
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/421,208
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/105,678
;      FILING DATE:  26-JUN-1998
;      APPLICATION NUMBER:  JP 172118/1997
;      FILING DATE:  27-JUN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Conlin, David G.
;      REGISTRATION NUMBER:  27,026
;      REFERENCE/DOCKET NUMBER:  48466-342
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-421-208-32

  Query Match             100.0%;  Score 172;  DB 3;  Length 32;
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  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 11
US-09-105-678A-33
; Sequence 33, Application US/09105678A
; Patent No. 6103882
;  GENERAL INFORMATION:
;    APPLICANT:  Suenaga, Masato
;    APPLICANT:  Moriya, Takeo
;    APPLICANT:  Tanaka, Yoko
;    APPLICANT:  Nishimura, Osamu
;    TITLE OF INVENTION:  METHOD OF PRODUCING A 19P2 LIGAND
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/105,678A
;      FILING DATE:  26-JUN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 172118/1997
;      FILING DATE:  27-JUN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Conlin, David G.
;      REGISTRATION NUMBER:  27,026
;      REFERENCE/DOCKET NUMBER:  48466-342
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-105-678A-33

  Query Match             100.0%;  Score 172;  DB 3;  Length 33;
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Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 12
US-08-776-971-7
; Sequence 7, Application US/08776971B
; Patent No. 6228984
;  GENERAL INFORMATION:
;       APPLICANT: Hinuma, Shuji
;                  Habata, Yugo
;                  Kawamata, Yuji
;                  Hosoya, Masaki
;                  Fujii, Ryo
;                  Fukusumi, Shoji
;                  Kitada, Chieko
;       TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
;       NUMBER OF SEQUENCES: 140
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;            STREET: 130 Water Street
;            CITY: Boston
;            STATE: MA
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;             COUNTRY: USA
;             ZIP: 02109
;          COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;          CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/776,971B
;             FILING DATE: 06-Feb-1997
;             CLASSIFICATION: <Unknown>
;          PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/JP96/03821
;             FILING DATE: 28-DEC-1996
;             APPLICATION NUMBER: JP 7/343371
;             FILING DATE: 28-DEC-1995
;             APPLICATION NUMBER: JP 8/59419
;             FILING DATE: 15-MAR-1996
;             APPLICATION NUMBER: JP 8/211805
;             FILING DATE: 12-AUG-1996
;             APPLICATION NUMBER: JP 8/246573
;             FILING DATE: 18-SEP-1996
;          ATTORNEY/AGENT INFORMATION:
;             NAME: Conlin, David G.
;             REGISTRATION NUMBER: 27,026
;             REFERENCE/DOCKET NUMBER: 47176
;          TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 617-523-3400
;             TELEFAX: 617-523-6440
;       INFORMATION FOR SEQ ID NO: 7:
;          SEQUENCE CHARACTERISTICS:
;             LENGTH: 33 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          FRAGMENT TYPE: internal
;          SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-776-971-7

  Query Match             100.0%;  Score 172;  DB 3;  Length 33;
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Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 13
US-09-421-208-33
; Sequence 33, Application US/09421208
; Patent No. 6258561
;  GENERAL INFORMATION:
;    APPLICANT:  Suenaga, Masato
;    APPLICANT:  Moriya, Takeo
;    APPLICANT:  Tanaka, Yoko
;    APPLICANT:  Nishimura, Osamu
;    TITLE OF INVENTION:  METHOD OF PRODUCING A 19P2 LIGAND
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/421,208
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/105,578
;      FILING DATE:  26-JUN-1998
;      APPLICATION NUMBER:  JP 172118/1997
;      FILING DATE:  27-JUN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Conlin, David G.
;      REGISTRATION NUMBER:  27,026
;      REFERENCE/DOCKET NUMBER:  48466-342
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-421-208-33

  Query Match             100.0%;  Score 172;  DB 3;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-19;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 14
US-08-776-971-1
; Sequence 1, Application US/08776971B
; Patent No. 6228984
;  GENERAL INFORMATION:
;       APPLICANT: Hinuma, Shuji
;                  Habata, Yugo
;                  Kawamata, Yuji
;                  Hosoya, Masaki
;                  Fujii, Ryo
;                  Fukusumi, Shoji
;                  Kitada, Chieko
;       TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
;       NUMBER OF SEQUENCES: 140
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;            STREET: 130 Water Street
;            CITY: Boston
;            STATE: MA
;            COUNTRY: USA
;            ZIP: 02109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/776,971B
;            FILING DATE: 06-Feb-1997
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: PCT/JP96/03821
;            FILING DATE: 28-DEC-1996
;            APPLICATION NUMBER: JP 7/343371
;            FILING DATE: 28-DEC-1995
;            APPLICATION NUMBER: JP 8/59419
;            FILING DATE: 15-MAR-1996
;            APPLICATION NUMBER: JP 8/211805
;            FILING DATE: 12-AUG-1996
;            APPLICATION NUMBER: JP 8/246573
;            FILING DATE: 18-SEP-1996
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; ATTORNEY/AGENT INFORMATION:
; NAME: Conlin, David G.
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 47176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-776-971-1

Query Match 100.0%; Score 172; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 5.1e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
Db 23 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 53

RESULT 15
US-08-776-971-44
; Sequence 44, Application US/08776971B
; Patent No. 6228984
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; Habata, Yugo
; Kawamata, Yuji
; Hosoya, Masaki
; Fujii, Ryo
; Fukusumi, Shoji
; Kitada, Chieko
; TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,971B
; FILING DATE: 06-Feb-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/03821
; FILING DATE: 28-DEC-1996
; APPLICATION NUMBER: JP 7/343371
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: JP 8/59419
; FILING DATE: 15-MAR-1996
; APPLICATION NUMBER: JP 8/211805
; FILING DATE: 12-AUG-1996
; APPLICATION NUMBER: JP 8/246573
; FILING DATE: 18-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Conlin, David G.
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 47176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-08-776-971-44

Query Match 100.0%; Score 172; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 5.1e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
Db 23 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 53

Search completed: November 12, 2003, 11:10:39
Job time : 22 secs

SEQ ID NO: 5
AC NO: US-08-776-971
Pat NO: 6228984; Database: Issued_Patents_AA

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Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 2
US-09-105-678A-31
; Sequence 31, Application US/09105678A
; Patent No. 6103882
;  GENERAL INFORMATION:
;    APPLICANT:  Suenaga, Masato
;    APPLICANT:  Moriya, Takeo
;    APPLICANT:  Tanaka, Yoko
;    APPLICANT:  Nishimura, Osamu
;    TITLE OF INVENTION:  METHOD OF PRODUCING A 19P2 LIGAND
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/105,678A
;      FILING DATE:  26-JUN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 172118/1997
;      FILING DATE:  27-JUN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Conlin, David G.
;      REGISTRATION NUMBER:  27,026
;      REFERENCE/DOCKET NUMBER:  48466-342
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-105-678A-31

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  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 3
US-08-776-971-5
; Sequence 5, Application US/08776971B
; Patent No. 6228984
;   GENERAL INFORMATION:
;        APPLICANT: Hinuma, Shuji
;                   Habata, Yugo
;                   Kawamata, Yuji
;                   Hosoya, Masaki
;                   Fujii, Ryo
;                   Fukusumi, Shoji
;                   Kitada, Chieko
;        TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
;        NUMBER OF SEQUENCES: 140
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;             STREET: 130 Water Street
;             CITY: Boston
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/776,971B
;             FILING DATE: 06-Feb-1997
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/JP96/03821
;             FILING DATE: 28-DEC-1996
;             APPLICATION NUMBER: JP 7/343371
;             FILING DATE: 28-DEC-1995
;             APPLICATION NUMBER: JP 8/59419
;             FILING DATE: 15-MAR-1996
;             APPLICATION NUMBER: JP 8/211805
;             FILING DATE: 12-AUG-1996
;             APPLICATION NUMBER: JP 8/246573
;             FILING DATE: 18-SEP-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Conlin, David G.
;             REGISTRATION NUMBER: 27,026
;             REFERENCE/DOCKET NUMBER: 47176
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 617-523-3400
;             TELEFAX: 617-523-6440
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 31 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        FRAGMENT TYPE: internal
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US-08-776-971-5

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Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 4
US-08-776-971-97
; Sequence 97, Application US/08776971B
; Patent No. 6228984
;   GENERAL INFORMATION:
;        APPLICANT: Hinuma, Shuji
;                   Habata, Yugo
;                   Kawamata, Yuji
;                   Hosoya, Masaki
;                   Fujii, Ryo
;                   Fukusumi, Shoji
;                   Kitada, Chieko
;        TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
;        NUMBER OF SEQUENCES: 140
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;             STREET: 130 Water Street
;             CITY: Boston
;             STATE: MA
;             COUNTRY: USA
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GenCore version 5.1.6

OM protein - protein search, using sw model

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Perfect score: 172
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	172	100.0	31	20	AAW97218	Bovine pituitary-d
3	172	100.0	31	20	AAW87613	Bovine 19P2 ligand
4	172	100.0	31	20	AAW95188	Bovine pituitary-d
5	172	100.0	31	21	AAB10347	Bovine oxytocin se
6	172	100.0	31	21	AAY49290	19P2 ligand peptid
7	172	100.0	31	21	AAY49298	19P2 ligand peptid
8	172	100.0	31	22	AAG62516	Bovine CRH releasi
9	172	100.0	31	23	AAE26399	Bovine PrRP-31 pep
10	172	100.0	31	24	ABU60825	Peptide production
11	172	100.0	31	24	ABU60831	Peptide production
12	172	100.0	32	18	AAW31372	Bovine G protein-c
13	172	100.0	32	20	AAW95189	Bovine pituitary-d
14	172	100.0	32	21	AAB10348	Bovine oxytocin se
15	172	100.0	32	22	AAG62517	Bovine CRH releasi
16	172	100.0	32	24	ABU60832	Peptide production
17	172	100.0	33	18	AAW31373	Bovine G protein-c
18	172	100.0	33	20	AAW95190	Bovine pituitary-d
19	172	100.0	33	21	AAB10349	Bovine oxytocin se
20	172	100.0	33	21	AAY49297	19P2 ligand peptid
21	172	100.0	33	22	AAG62518	Bovine CRH releasi
22	172	100.0	33	24	ABU60833	Peptide production
23	172	100.0	98	18	AAW31382	Bovine genome deri
24	172	100.0	98	18	AAW31368	Bovine G protein-c
25	172	100.0	98	20	AAW97224	Bovine genome-driv
26	172	100.0	98	20	AAW97217	Bovine pituitary-d
27	172	100.0	98	20	AAW95187	Bovine genome-deri
28	172	100.0	98	21	AAB10346	Bovine oxytocin se
29	172	100.0	98	21	AAB10353	Bovine oxytocin se
30	172	100.0	98	22	AAG62515	Bovine CRH releasi
31	172	100.0	98	22	AAG62522	Bovine CRH releasi
32	166	96.5	31	22	AAB90995	Prolactin releasin
33	164	95.3	31	22	AAB73370	bPrRp31 peptide, u
34	163	94.8	31	18	AAW31384	Rat type G protein
35	163	94.8	31	20	AAW97233	Rat type ligand pc
36	163	94.8	31	20	AAW87614	Rat 19P2 ligand.
37	163	94.8	31	20	AAW95173	Murine pituitary-d
38	163	94.8	31	20	AAW95174	Murine pituitary-d
39	163	94.8	31	21	AAB10355	Rat oxytocin secre
40	163	94.8	31	21	AAY87504	Rat prolactin-rele
41	163	94.8	31	21	AAY49292	19P2 ligand peptid
42	163	94.8	31	22	AAG62524	Rat CRH releasing
43	163	94.8	31	22	AAB90993	Prolactin releasin
44	163	94.8	31	23	AAE26400	Rat PrRP-31 peptid
45	163	94.8	31	24	ABU60826	Peptide production

ALIGNMENTS

RESULT 1
AAW31371
ID AAW31371 standard; Peptide; 31 AA.
XX
AC AAW31371;
XX
DT 06-APR-1998 (first entry)
XX
DE Bovine G protein-coupled receptor ligand peptide fragment 1.
XX
KW G protein-coupled receptor; ligand binding; pharmaceutical;
KW modulator; pituitary; central nervous system; pancreas; prophylactic;
KW therapeutic agent.
XX
OS Bos taurus.
XX
PN WO9724436-A2.
XX
PD 10-JUL-1997.
XX
PF 26-DEC-1996; 96WO-JP03821.
XX
PR 18-SEP-1996; 96JP-0246573.
PR 28-DEC-1995; 95JP-0343371.
PR 15-MAR-1996; 96JP-0059419.
PR 12-AUG-1996; 96JP-0211805.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Fujii R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;
PI Kawamata Y, Kitada C;
XX

DR WPI; 1997-363672/33.
DR N-PSDB; AAV02394.
XX
PT Ligand peptide for G protein-coupled receptor - acts by modulating
PT function in the central nervous system, pancreas and pituitary gland
XX
PS Claim 2; Page 160; 258pp; English.
XX
CC This sequence represents a peptide fragment of a novel bovine pituitary
CC derived ligand corresponding to amino acid residues 23 to 53 of the
CC sequence in AAW31368 and is used in an assay to monitor ligand binding
CC to the G protein-coupled receptor protein. Pharmaceutical compositions
CC containing this ligand may be used as a pituitary function modulator, a
CC central nervous system modulator or a pancreatic function modulator.
CC This ligand could have specific applications as a prophylactic or
CC therapeutic agent for dementia, depression, hyperkinetic syndrome,
CC disturbance of consciousness, anxiety syndrome, schizophrenia, trauma,
CC growth hormone secretory disease, hyper- and polyphagia,
CC hypercholesterolaemia, hyperglyceridaemia, hyperlipidaemia,
CC hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease,
CC Turner's syndrome, neurosis, rheumatoid arthritis, spinal injury,
CC transient brain ischaemia, amylotrophic lateral sclerosis, acute
CC myocardial infarction, spinocerebellar degeneration, bone fracture,
CC trauma, atopic dermatitis, osteoporosis, asthma, epilepsy, infertility
CC and/or oligogalactia. Assays can also be developed to screen compounds
CC which are capable of altering the binding activity of the ligand thus
CC affecting activation of the G protein-coupled receptor protein.
XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 172; DB 18; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
Db 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 2
AAW97218
ID AAW97218 standard; peptide; 31 AA.
XX
AC AAW97218;
XX
DT 06-MAY-1999 (first entry)
XX
DE Bovine pituitary-derived ligand polypeptide fragment.
XX
KW Bovine pituitary-derived ligand; modulation; prolactin secretion;
KW G protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis;
KW menopausal syndrome; euthyroid; hypometabolism; lactation;
KW pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease;
KW prolactinoma; infertility; impotence; amenorrhea; galactorrhea;
KW acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome;
KW Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia;
KW contraceptive; placental function; choriocarcinoma; hydatid mole;
KW irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism;
KW abnormal lipidmetabolism; oxytocia.
XX
OS Bos sp.
XX
PN WO9858962-A1.
XX
PD 30-DEC-1998.
XX
PF 22-JUN-1998; 98WO-JP02765.
XX
PR 23-JUN-1997; 97JP-0165437.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Fujii R, Hinuma S, Kawamata Y, Matsumoto H;

XX
DR WPI; 1999-105614/09.
XX
PT Use of G protein-coupled receptor ligands - for modulating prolactin
PT secretion or placental function, e.g. for treating menopausal
PT syndrome, tumours, autoimmune disease or abnormal pregnancy
XX
PS Claim 3; Page 135; 241pp; English.
XX
CC The present sequence represents a bovine pituitary-derived ligand
CC fragment. It is used in the course of the invention. The specification
CC describes an agent for modulating prolactin secretion which comprises a
CC ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR)
CC protein. The agents for promoting prolactin secretion can be used for
CC treating or preventing hypoovarianism, gonecyst cacogenesis, menopausal
CC syndrome, euthyroid or hypometabolism. They can by used for promoting
CC lactation in a domestic mammal and as an aphrodisiac. The agents for
CC inhibiting prolactin secretion can be used for treating or preventing
CC pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease,
CC prolactinoma, infertility, impotence, amenorrhea, galactorrhea,
CC acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome,
CC Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia.
CC The inhibitory agents can also be used as contraceptives. The agents for
CC modulating placental function can be used for treating or preventing
CC choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus,
CC abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 172; DB 20; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
Db 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 3
AAW87613
ID AAW87613 standard; Peptide; 31 AA.
XX
AC AAW87613;
XX
DT 29-MAR-1999 (first entry)
XX
DE Bovine 19P2 ligand.
XX
KW 19P2 ligand; G protein coupled receptor; pituitary;
KW prolactin releasing peptide; cattle; dementia; breast cancer;
KW therapy.
XX
OS Bos taurus.
XX
PN EP887417-A2.
XX
PD 30-DEC-1998.
XX
PF 25-JUN-1998; 98EP-0111725.
XX
PR 27-JUN-1997; 97JP-0172118.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Moriya T, Nishimura O, Suenaga M, Tanaka Y;
XX
DR WPI; 1999-047884/05.
XX
PT Producing a 19P2 pituitary G protein receptor ligand - by cleavage
PT of a fusion protein, useful for preventing and treating dementia,
PT breast cancer, renal failure and autoimmune disease
XX
PS Claim 5; Page 34; 56pp; English.

```
XX
CC   This is the amino acid sequence of the bovine pituitary G
CC   protein-coupled receptor ligand 19P2L.  A method suitable for
CC   commercial high-level production of 19P2L comprises expressing
CC   the ligand in host cells as a recombinant fusion protein e.g. with
CC   human basic fibroblast growth factor (see AAV83792-93) that has
CC   been modified to include an N-terminal cysteine residue.  The
CC   ligand is released from the fusion by cyanylation followed by
CC   ammonolysis.  19P2L has prolactin secretion-stimulating and (at
CC   high doses) prolactin secretion-inhibiting properties.  It can be
CC   used in the treatment and prevention of various diseases including:
CC   senile dementia, cerebrovascular dementia, and dementia associated
CC   with: genealogical disorders (e.g. Alzheimer's disease, Parkinson's
CC   disease, Pick's disease, Huntington's disease), infectious diseases
CC   (e.g. Creutzfeldt-Jakob's), endocrine or metabolic disease or
CC   toxicosis (e.g. hypothyroidism, vitamin B12 deficiency, alcoholism,
CC   intoxication by drugs, metal and organic compounds), tumourigenic
CC   diseases (e.g. brain tumour), traumatic diseases (e.g. chronic
CC   subarachnoidal heamorrhage, and other types of dementia, depression,
CC   hyperactive child syndrome (microencephalopathy) and disturbance of
CC   consciousness.  It is also useful for prevention and treatment of
CC   diseases associated with prolactin hypo and hypersecretion
CC   respectively, including: hyperprolactinaemia, pituitary adenoma,
CC   breast cancer, infertility, impotence and autoimmune disease
CC   (hypersecretion disorders), and seminal vesicle hypoplasia,
CC   osteoporosis, menopausal syndrome and renal failure (hyposecretion
CC   disorders).  The 19P2 polypeptide/amide is also useful as a test
CC   reagent for study of the prolactin secretory function or as a
CC   lactogogue in mammalian farm animals.
XX
SQ   Sequence   31 AA;

  Query Match             100.0%;  Score 172;  DB 20;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-18;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 4
AAW95188
ID   AAW95188 standard; peptide; 31 AA.
XX
AC   AAW95188;
XX
DT   10-MAR-1999  (first entry)
XX
DE   Bovine pituitary-derived ligand polypeptide fragment.
XX
KW   Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor;
KW   GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas;
KW   tissue; screen; therapeutic; binding; senile dementia; ligand; murine;
KW   Alzheimer's disease; Parkinson's disease; Huntington's disease; drug;
KW   Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone;
KW   secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;
KW   gene therapy; transgenic animal; bovine.
XX
OS   Bos sp.
XX
PN   WO9849295-A1.
XX
PD   05-NOV-1998.
XX
PF   27-APR-1998;   98WO-JP01923.
XX
PR   28-APR-1997;   97JP-0109974.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Fukusumi S,  Hinuma S;
XX
DR   WPI; 1999-009423/01.
XX
PT   New polypeptide ligand for orphan G protein coupled receptors - used
PT   for treating disorders of central nervous system, pituitary and
PT   pancreas, and for drug screening
XX
PS   Example 19; Page 150; 206pp; English.
XX
CC   The invention relates to a murine pituitary-derived ligand polypeptide
CC   which is a ligand for the G-protein coupled orphan receptor designated
CC   GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing
CC   the ligand polypeptide encoding DNA are used to produce a recombinant
CC   ligand polypeptide. The ligand polypeptide, and its fragments, modulate
CC   function of the pituitary, central nervous system, pancreas and other
CC   tissues and can be used to screen for agents that modulate binding of the
CC   polypeptide to the receptor; to quantify the amount of receptor in a
CC   sample and to raise antibodies. They may also be used therapeutically,
CC   e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's
CC   diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs;
CC   diabetes; schizophrenia; disorders of growth hormone secretion; cancer;
CC   rheumatoid arthritis, epilepsy and many others, also to improve post-
CC   operative nutritional status and as vasopressor. Transgenic animals
CC   carrying the ligand polypeptide encoding DNA or its mutein are used to
CC   study the function of the polypeptide-expressing genes, as models of
CC   disease, for drug screening and as source of cell lines. The ligand
CC   polypeptide DNA is used as a source of probes and primers; to identify
CC   related sequences; in receptor-binding assays; for production of Ab and
CC   antisera; in drug development; for gene therapy and to develop transgenic
CC   animals. The present sequence represents a bovine genome-derived ligand
CC   polypeptide fragment which is similar to the murine ligand-polypeptide.
XX
SQ   Sequence   31 AA;

  Query Match             100.0%;  Score 172;  DB 20;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-18;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 5
AAB10347
ID   AAB10347 standard; peptide; 31 AA.
XX
AC   AAB10347;
XX
DT   24-NOV-2000  (first entry)
XX
DE   Bovine oxytocin secretion promoting peptide SEQ ID NO: 3.
XX
KW   Bovine; oxytocin secretion promoter; G protein-coupled receptor protein;
KW   treatment; disease; pain; atonic bleeding; uterine recovery failure; cow;
KW   caesarean section; artificial fertilization; galactostasis; goat; pig;
KW   veterinary medicine; milk production.
XX
OS   Bos taurus.
XX
PN   WO200038704-A1.
XX
PD   06-JUL-2000.
XX
PF   22-DEC-1999;   99WO-JP07199.
XX
PR   25-DEC-1998;   98JP-0369585.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Matsumoto H,  Kitada C,  Hinuma S;
XX
DR   WPI; 2000-452298/39.
XX
```

```
PT   Physiologically-active polypeptide recognized as ligand by G
PT   protein-coupled receptor protein, for promoting secretion of oxytocin,
PT   as drugs for diseases relating to oxytocin secretion and in veterinary
PT   medicine -
XX
PS   Claim 3; Page 50; 72pp; Japanese.
XX
CC   This invention describes a novel oxytocin secretion-regulating agent
CC   which contains a ligand peptide or its salt for the G protein-coupled
CC   receptor protein. It is useful in the form of drugs for ameliorating,
CC   preventing and treating diseases relating to oxytocin secretion e.g.
CC   weak pains and atonic bleeding, before and after expulsion of placenta,
CC   uterine recovery failure, caesarean section, stoppage of artificial
CC   fertilization or galactostasis and is also applicable in veterinary
CC   medicine for promoting milk production in cow, goat and pig. This
CC   sequence represents a bovine peptide which acts as an oxytocin secretion
CC   promoter.
XX
SQ   Sequence   31 AA;

  Query Match             100.0%;  Score 172;  DB 21;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-18;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 6
AAY49290
ID   AAY49290 standard; peptide; 31 AA.
XX
AC   AAY49290;
XX
DT   22-FEB-2000  (first entry)
XX
DE   19P2 ligand peptide fragment.
XX
KW   Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion;
KW   pituitary; regulatory mechanism; central nervous system; pancreatic.
XX
OS   Bos sp.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   31
FT                   /note= "C-terminal amide"
XX
PN   WO9960112-A1.
XX
PD   25-NOV-1999.
XX
PF   20-MAY-1999;   99WO-JP02650.
XX
PR   21-MAY-1998;   98JP-0140293.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Matsumoto H,  Kitada C,  Hinuma S;
XX
DR   WPI; 2000-039381/03.
XX
PT   New monoclonal antibodies,  useful in diagnosis, as drugs and  in
PT   studying diseases related to ligand abnormality  -
XX
PS   Disclosure; Page 26; 73pp; Japanese.
XX
CC   The invention provides a monoclonal antibody which has a specific
CC   reaction with the part peptide of the C-terminal of 19P2 ligand or its
CC   derivative. The antibodies can be used in diagnosis or to treat or
CC   prevent diseases associated with abnormality in the pituitary function
CC   regulatory mechanism (e.g. promotion of prolactin secretion), central
CC   nervous regulatory mechanism, and pancreatic function regulatory
CC   mechanism. The antibody-based immunoassay can also be applied in
CC   clarifying the physiological functions of the ligand and its derivative.
CC   Sequences AAY49290-302 represent peptide fragments of the 19P2 ligand.
XX
SQ   Sequence   31 AA;

  Query Match             100.0%;  Score 172;  DB 21;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-18;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 7
AAY49298
ID   AAY49298 standard; peptide; 31 AA.
XX
AC   AAY49298;
XX
DT   22-FEB-2000  (first entry)
XX
DE   19P2 ligand peptide fragment.
XX
KW   Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion;
KW   pituitary; regulatory mechanism; central nervous system; pancreatic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   31
FT                   /note= "C-terminal amide"
XX
PN   WO9960112-A1.
XX
PD   25-NOV-1999.
XX
PF   20-MAY-1999;   99WO-JP02650.
XX
PR   21-MAY-1998;   98JP-0140293.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Matsumoto H,  Kitada C,  Hinuma S;
XX
DR   WPI; 2000-039381/03.
XX
PT   New monoclonal antibodies,  useful in diagnosis, as drugs and  in
PT   studying diseases related to ligand abnormality  -
XX
PS   Disclosure; Page 27; 73pp; Japanese.
XX
CC   The invention provides a monoclonal antibody which has a specific
CC   reaction with the part peptide of the C-terminal of 19P2 ligand or its
CC   derivative. The antibodies can be used in diagnosis or to treat or
CC   prevent diseases associated with abnormality in the pituitary function
CC   regulatory mechanism (e.g. promotion of prolactin secretion), central
CC   nervous regulatory mechanism, and pancreatic function regulatory
CC   mechanism. The antibody-based immunoassay can also be applied in
CC   clarifying the physiological functions of the ligand and its derivative.
CC   Sequences AAY49290-302 represent peptide fragments of the 19P2 ligand.
XX
SQ   Sequence   31 AA;

  Query Match             100.0%;  Score 172;  DB 21;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-18;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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```
RESULT 8
AAG62516
ID   AAG62516 standard; peptide; 31 AA.
XX
AC   AAG62516;
XX
DT   24-AUG-2001  (first entry)
XX
DE   Bovine CRH releasing protein related peptide SEQ ID NO: 3.
XX
KW   Cow; corticotrophin releasing hormone; CRH; G protein receptor ligand;
KW   analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism;
KW   Addison's disease; adrenal gland hyperfunction; obesity.
XX
OS   Bos taurus.
XX
PN   WO200135984-A1.
XX
PD   25-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-JP08119.
XX
PR   18-NOV-1999;   99JP-0327900.
PR   26-SEP-2000; 2000JP-0297073.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Kitada C,  Matsumoto H,  Hinuma S;
XX
DR   WPI; 2001-355552/37.
XX
PT   Use of G protein receptor ligand or peptide for controlling
PT   corticotropin releasing hormone secretion -
XX
PS   Claim 3; Page 63; 90pp; Japanese.
XX
CC   The present sequence describes a method of controlling the secretion of
CC   corticotrophin releasing hormone (CRH), involving the use of a G protein
CC   receptor ligand. This can be used to control the secretion of CRH and is
CC   useful as an analgesic or for treating, preventing or ameliorating
CC   diseases associated with CRH secretion such as hyperaldosteronism,
CC   hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's
CC   disease (including boredom, nausea, pigmentation, hypogonadism, hair
CC   loss, and hypotension), adrenal gland hypofunction and obesity. The
CC   present sequence is a peptide used in the exemplification of the
CC   invention.
XX
SQ   Sequence   31 AA;

  Query Match            100.0%;  Score 172;  DB 22;  Length 31;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-18;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 9
AAE26399
ID   AAE26399 standard; peptide; 31 AA.
XX
AC   AAE26399;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Bovine PrRP-31 peptide.
XX
KW   Wakefulness; sleep disorder; prolactin releasing peptide receptor;
KW   PrRP; GPR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea;
KW   insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure;
KW   anticonvulsant; bovine.
XX
OS   Bos taurus.
XX
PN   US2002037533-A1.
XX
PD   28-MAR-2002.
XX
PF   17-AUG-2001; 2001US-0932161.
XX
PR   28-APR-2000; 2000US-0560915.
XX
PA   (CIVE/) CIVELLI O.
PA   (LINS/) LIN S.
XX
PI   Civelli O,  Lin S;
XX
DR   WPI; 2002-403931/43.
XX
PT   Screening for compounds useful for promoting wakefulness or sleep, and
PT   for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep
PT   apnea, comprises administering a prolactin releasing peptide agonist or
PT   antagonist  -
XX
PS   Disclosure; Page 24; 35pp; English.
XX
CC   The present invention relates to a method of screening for compounds
CC   for promoting wakefulness or sleep in a mammal. The method involves
CC   administering a prolactin releasing peptide (PrRP) receptor (GPR10)
CC   agonist or antagonist respectively and determining the ability of the
CC   compound to promote wakefulness or sleep. The compounds identified
CC   from the method are used in the therapy of epilepsy and other diseases
CC   associated with absence seizures and in promoting wakefulness and sleep
CC   in individuals having sleep disorders such as insomnia and narcolepsy.
CC   PrRP receptor agonists may be used to treat common disorders which lead
CC   to sleepiness, e.g. sleep apnoea, narcolepsy, idiopathic hypersomnia
CC   and psychogenic hypersomnia. PrRP receptor antagonists are useful for
CC   promoting sleep and for treating insomnia such as adjustment sleep
CC   disorder and psychophysiologic insomnia. The present sequence is bovine
CC   PrRP-31 peptide.
XX
SQ   Sequence   31 AA;

  Query Match            100.0%;  Score 172;  DB 23;  Length 31;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-18;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 10
ABU60825
ID   ABU60825 standard; Peptide; 31 AA.
XX
AC   ABU60825;
XX
DT   06-MAY-2003  (first entry)
XX
DE   Peptide production by gene recombination associated peptide #9.
XX
KW   Peptide production; low-molecular peptide; KiSS-1; GPR8 ligand;
KW   gene recombination.
XX
OS   Bos sp.
XX
PN   WO200292829-A1.
XX
PD   21-NOV-2002.
XX
PF   16-MAY-2002; 2002WO-JP04735.
XX
PR   17-MAY-2001; 2001JP-0147341.
```

XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Nishimura O, Suenaga M, Ito T, Kitada C;
XX
DR WPI; 2003-129302/12.
XX
PT Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for
PT subsequent applications by gene recombination technique through tandem
PT repeats to provide precursor protein with specific cleavage sites -
XX
PS Disclosure; Page 58; 87pp; Japanese.
XX
CC The invention describes a method of producing a peptide comprising the
CC excision of the N and C-terminals of a target peptide with enzymes or
CC chemically through the attached cleavage sites repeated by ligation in a
CC precursor protein. The method is for producing (low-molecular) peptides
CC e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by the
CC gene recombination technique through tandem repeats to provide
CC a precursor protein with specific cleavage sites. With this method,
CC peptide production can be carried out easily to provide large quantities
CC of the required peptides. This is the amino acid sequence of a peptide
CC associated with the peptide production method of the invention.
XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 172; DB 24; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
Db 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 11
ABU60831
ID ABU60831 standard; Peptide; 31 AA.
XX
AC ABU60831;
XX
DT 06-MAY-2003 (first entry)
XX
DE Peptide production by gene recombination associated peptide #15.
XX
KW Peptide production; low-molecular peptide; KiSS-1; GPR8 ligand;
KW gene recombination.
XX
OS Bos sp.
XX
PN WO200292829-A1.
XX
PD 21-NOV-2002.
XX
PF 16-MAY-2002; 2002WO-JP04735.
XX
PR 17-MAY-2001; 2001JP-0147341.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Nishimura O, Suenaga M, Ito T, Kitada C;
XX
DR WPI; 2003-129302/12.
XX
PT Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for
PT subsequent applications by gene recombination technique through tandem
PT repeats to provide precursor protein with specific cleavage sites -
XX
PS Disclosure; Page 61; 87pp; Japanese.
XX
CC The invention describes a method of producing a peptide comprising the
CC excision of the N and C-terminals of a target peptide with enzymes or
CC chemically through the attached cleavage sites repeated by ligation in a
CC precursor protein. The method is for producing (low-molecular) peptides
CC e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by the
CC gene recombination technique through tandem repeats to provide
CC a precursor protein with specific cleavage sites. With this method,
CC peptide production can be carried out easily to provide large quantities
CC of the required peptides. This is the amino acid sequence of a peptide
CC associated with the peptide production method of the invention.
XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 172; DB 24; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
Db 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 12
AAW31372
ID AAW31372 standard; Peptide; 32 AA.
XX
AC AAW31372;
XX
DT 06-APR-1998 (first entry)
XX
DE Bovine G protein-coupled receptor ligand peptide fragment 2.
XX
KW G protein-coupled receptor; ligand binding; pharmaceutical;
KW modulator; pituitary; central nervous system; pancreas; prophylactic;
KW therapeutic agent.
XX
OS Bos taurus.
XX
PN WO9724436-A2.
XX
PD 10-JUL-1997.
XX
PF 26-DEC-1996; 96WO-JP03821.
XX
PR 18-SEP-1996; 96JP-0246573.
PR 28-DEC-1995; 95JP-0343371.
PR 15-MAR-1996; 96JP-0059419.
PR 12-AUG-1996; 96JP-0211805.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Fujii R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;
PI Kawamata Y, Kitada C;
XX
DR WPI; 1997-363672/33.
DR N-PSDB; AAV02395.
XX
PT Ligand peptide for G protein-coupled receptor - acts by modulating
PT function in the central nervous system, pancreas and pituitary gland
XX
PS Claim 2; Page 160-161; 258pp; English.
XX
CC This sequence represents a peptide fragment of a novel bovine pituitary
CC derived ligand corresponding to amino acid residues 23 to 54 of the
CC sequence in AAW31368 and is used in an assay to monitor ligand binding
CC to the G protein-coupled receptor protein. Pharmaceutical compositions
CC containing this ligand may be used as a pituitary function modulator, a
CC central nervous system modulator or a pancreatic function modulator.
CC This ligand could have specific applications as a prophylactic or
CC therapeutic agent for dementia, depression, hyperkinetic syndrome,
CC disturbance of consciousness, anxiety syndrome, schizophrenia, trauma,
CC growth hormone secretory disease, hyper- and polyphagia,
CC hypercholesterolaemia, hyperglyceridaemia, hyperlipidaemia,
CC hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease,
CC Turner's syndrome, neurosis, rheumatoid arthritis, spinal injury,
CC transient brain ischaemia, amyotrophic lateral sclerosis, acute

```
CC   myocardial infarction, spinocerebellar degeneration, bone fracture,
CC   trauma, atopic dermatitis, osteoporosis, asthma, epilepsy, infertility
CC   and/or oligogalactia. Assays can also be developed to screen compounds
CC   which are capable of altering the binding activity of the ligand thus
CC   affecting activation of the G protein-coupled receptor protein.
XX
SQ   Sequence   32 AA;

  Query Match           100.0%;  Score 172;  DB 18;  Length 32;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-18;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              |||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 13
AAW95189
ID   AAW95189 standard; peptide; 32 AA.
XX
AC   AAW95189;
XX
DT   10-MAR-1999  (first entry)
XX
DE   Bovine pituitary-derived ligand polypeptide fragment.
XX
KW   Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor;
KW   GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas;
KW   tissue; screen; therapeutic; binding; senile dementia; ligand; murine;
KW   Alzheimer's disease; Parkinson's disease; Huntington's disease; drug;
KW   Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone;
KW   secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;
KW   gene therapy; transgenic animal; bovine.
XX
OS   Bos sp.
XX
PN   WO9849295-A1.
XX
PD   05-NOV-1998.
XX
PF   27-APR-1998;   98WO-JP01923.
XX
PR   28-APR-1997;   97JP-0109974.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Fukusumi S,  Hinuma S;
XX
DR   WPI; 1999-009423/01.
XX
PT   New polypeptide ligand for orphan G protein coupled receptors - used
PT   for treating disorders of central nervous system, pituitary and
PT   pancreas, and for drug screening
XX
PS   Example 19; Page 150; 206pp; English.
XX
CC   The invention relates to a murine pituitary-derived ligand polypeptide
CC   which is a ligand for the G-protein coupled orphan receptor designated
CC   GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing
CC   the ligand polypeptide encoding DNA are used to produce a recombinant
CC   ligand polypeptide. The ligand polypeptide, and its fragments, modulate
CC   function of the pituitary, central nervous system, pancreas and other
CC   tissues and can be used to screen for agents that modulate binding of the
CC   polypeptide to the receptor; to quantify the amount of receptor in a
CC   sample and to raise antibodies. They may also be used therapeutically,
CC   e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's
CC   diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs;
CC   diabetes; schizophrenia; disorders of growth hormone secretion; cancer;
CC   rheumatoid arthritis, epilepsy and many others, also to improve post-
CC   operative nutritional status and as vasopressor. Transgenic animals
CC   carrying the ligand polypeptide encoding DNA or its mutein are used to
CC   study the function of the polypeptide-expressing genes, as models of
CC   disease, for drug screening and as source of cell lines. The ligand
CC   polypeptide DNA is used as a source of probes and primers; to identify
CC   related sequences; in receptor-binding assays; for production of Ab and
CC   antisera; in drug development; for gene therapy and to develop transgenic
CC   animals. The present sequence represents a bovine genome-derived ligand
CC   polypeptide fragment which is similar to the murine ligand-polypeptide.
XX
SQ   Sequence   32 AA;

  Query Match           100.0%;  Score 172;  DB 20;  Length 32;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-18;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 14
AAB10348
ID   AAB10348 standard; peptide; 32 AA.
XX
AC   AAB10348;
XX
DT   24-NOV-2000  (first entry)
XX
DE   Bovine oxytocin secretion promoting peptide SEQ ID NO: 4.
XX
KW   Bovine; oxytocin secretion promoter; G protein-coupled receptor protein;
KW   treatment; disease; pain; atonic bleeding; uterine recovery failure; cow;
KW   caesarean section; artificial fertilization; galactostasis; goat; pig;
KW   veterinary medicine; milk production.
XX
OS   Bos taurus.
XX
PN   WO200038704-A1.
XX
PD   06-JUL-2000.
XX
PF   22-DEC-1999;   99WO-JP07199.
XX
PR   25-DEC-1998;   98JP-0369585.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Matsumoto H,  Kitada C,  Hinuma S;
XX
DR   WPI; 2000-452298/39.
XX
PT   Physiologically-active polypeptide recognized as ligand by G
PT   protein-coupled receptor protein, for promoting secretion of oxytocin,
PT   as drugs for diseases relating to oxytocin secretion and in veterinary
PT   medicine -
XX
PS   Disclosure; Page 51; 72pp; Japanese.
XX
CC   This invention describes a novel oxytocin secretion-regulating agent
CC   which contains a ligand peptide or its salt for the G protein-coupled
CC   receptor protein. It is useful in the form of drugs for ameliorating,
CC   preventing and treating diseases relating to oxytocin secretion e.g.
CC   weak pains and atonic bleeding, before and after expulsion of placenta,
CC   uterine recovery failure, caesarean section, stoppage of artificial
CC   fertilization or galactostasis and is also applicable in veterinary
CC   medicine for promoting milk production in cow, goat and pig. This
CC   sequence represents a bovine peptide which acts as an oxytocin secretion
CC   promoter.
XX
SQ   Sequence   32 AA;

  Query Match           100.0%;  Score 172;  DB 21;  Length 32;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-18;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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RESULT 15
AAG62517
ID AAG62517 standard; peptide; 32 AA.
XX
AC AAG62517;
XX
DT 24-AUG-2001 (first entry)
XX
DE Bovine CRH releasing protein related peptide SEQ ID NO: 4.
XX
KW Cow; corticotrophin releasing hormone; CRH; G protein receptor ligand;
KW analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism;
KW Addison's disease; adrenal gland hyperfunction; obesity.
XX
OS Bos taurus.
XX
PN WO200135984-A1.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-JP08119.
XX
PR 18-NOV-1999; 99JP-0327900.
PR 26-SEP-2000; 2000JP-0297073.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Kitada C, Matsumoto H, Hinuma S;
XX
DR WPI; 2001-355552/37.
XX
PT Use of G protein receptor ligand or peptide for controlling
PT corticotropin releasing hormone secretion -
XX
PS Disclosure; Page 64; 90pp; Japanese.
XX
CC The present sequence describes a method of controlling the secretion of
CC corticotrophin releasing hormone (CRH), involving the use of a G protein
CC receptor ligand. This can be used to control the secretion of CRH and is
CC useful as an analgesic or for treating, preventing or ameliorating
CC diseases associated with CRH secretion such as hyperaldosteronism,
CC hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's
CC disease (including boredom, nausea, pigmentation, hypogonadism, hair
CC loss, and hypotension), adrenal gland hypofunction and obesity. The
CC present sequence is a peptide used in the exemplification of the
CC invention.
XX
SQ Sequence 32 AA;

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  Query Match            100.0%;  Score 172;  DB 22;  Length 32;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-18;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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Job time : 41 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 12, 2003, 11:08:23 ; Search time 172 Seconds
(without alignments)
163.997 Million cell updates/sec

Title: US-09-446-543A-5
Perfect score: 172
Sequence: 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	172	100.0	31	1	PCT-US02-24248-13	Sequence 13, Appl
2	172	100.0	31	15	US-09-105-678-7	Sequence 7, Appli
3	172	100.0	31	15	US-09-105-678-31	Sequence 31, Appl
4	172	100.0	31	18	US-09-403-639A-39	Sequence 39, Appl
5	172	100.0	31	18	US-09-403-639B-39	Sequence 39, Appl
6	172	100.0	31	18	US-09-403-639C-39	Sequence 39, Appl
7	172	100.0	31	18	US-09-446-543A-5	Sequence 5, Appli
8	172	100.0	31	19	US-09-576-290-5	Sequence 5, Appli
9	172	100.0	31	19	US-09-576-290-97	Sequence 97, Appl
10	172	100.0	31	21	US-09-716-147-5	Sequence 5, Appli
11	172	100.0	31	21	US-09-716-147-97	Sequence 97, Appl
12	172	100.0	31	23	US-09-868-885B-3	Sequence 3, Appli
13	172	100.0	31	24	US-09-932-161-13	Sequence 13, Appl
14	172	100.0	31	26	US-10-044-592-39	Sequence 39, Appl
15	172	100.0	31	26	US-10-096-777-13	Sequence 13, Appl
16	172	100.0	31	27	US-10-130-584-3	Sequence 3, Appli
17	172	100.0	32	15	US-09-105-678-32	Sequence 32, Appl
18	172	100.0	32	18	US-09-403-639A-40	Sequence 40, Appl
19	172	100.0	32	18	US-09-403-639B-40	Sequence 40, Appl
20	172	100.0	32	18	US-09-403-639C-40	Sequence 40, Appl
21	172	100.0	32	18	US-09-446-543A-6	Sequence 6, Appli
22	172	100.0	32	19	US-09-576-290-6	Sequence 6, Appli
23	172	100.0	32	21	US-09-716-147-6	Sequence 6, Appli
24	172	100.0	32	23	US-09-868-885B-4	Sequence 4, Appli
25	172	100.0	32	26	US-10-044-592-40	Sequence 40, Appl
26	172	100.0	32	27	US-10-130-584-4	Sequence 4, Appli
27	172	100.0	33	15	US-09-105-678-33	Sequence 33, Appl
28	172	100.0	33	18	US-09-403-639A-41	Sequence 41, Appl
29	172	100.0	33	18	US-09-403-639B-41	Sequence 41, Appl
30	172	100.0	33	18	US-09-403-639C-41	Sequence 41, Appl
31	172	100.0	33	18	US-09-446-543A-7	Sequence 7, Appli
32	172	100.0	33	19	US-09-576-290-7	Sequence 7, Appli
33	172	100.0	33	21	US-09-700-643A-8	Sequence 8, Appli
34	172	100.0	33	21	US-09-716-147-7	Sequence 7, Appli
35	172	100.0	33	23	US-09-868-885B-5	Sequence 5, Appli
36	172	100.0	33	26	US-10-044-592-41	Sequence 41, Appl
37	172	100.0	33	27	US-10-130-584-5	Sequence 5, Appli
38	172	100.0	98	18	US-09-403-639A-28	Sequence 28, Appl
39	172	100.0	98	18	US-09-403-639A-38	Sequence 38, Appl
40	172	100.0	98	18	US-09-403-639B-28	Sequence 28, Appl
41	172	100.0	98	18	US-09-403-639B-38	Sequence 38, Appl
42	172	100.0	98	18	US-09-403-639B-82	Sequence 82, Appl
43	172	100.0	98	18	US-09-403-639B-84	Sequence 84, Appl
44	172	100.0	98	18	US-09-403-639B-86	Sequence 86, Appl
45	172	100.0	98	18	US-09-403-639B-88	Sequence 88, Appl

ALIGNMENTS

RESULT 1
PCT-US02-24248-13
; Sequence 13, Application PC/TUS0224248
; GENERAL INFORMATION:
; APPLICANT: Civelli, Olivier
; APPLICANT: Lin, Steven
; TITLE OF INVENTION: Screening and Therapeutic Methods For
; TITLE OF INVENTION: Promoting Wakefulness and Sleep
; FILE REFERENCE: P-UC 4679
; CURRENT APPLICATION NUMBER: PCT/US02/24248
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/560,915
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Bos taurus
PCT-US02-24248-13

Query Match 100.0%; Score 172; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.1e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 2
US-09-105-678-7
; Sequence 7, Application US/09105678
;  GENERAL INFORMATION:
;    APPLICANT:  Suenaga, Masato
;    APPLICANT:  Moriya, Takeo
;    APPLICANT:  Tanaka, Yoko
;    APPLICANT:  Nishimura, Osamu
;    TITLE OF INVENTION:  METHOD OF PRODUCING A 19P2 LIGAND
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/105,678
;      FILING DATE:  26-JUN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 172118/1997
;      FILING DATE:  27-JUN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Conlin, David G.
;      REGISTRATION NUMBER:  27,026
;      REFERENCE/DOCKET NUMBER:  48466-342
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-105-678-7

  Query Match             100.0%;  Score 172;  DB 15;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-17;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 3
US-09-105-678-31
; Sequence 31, Application US/09105678
;  GENERAL INFORMATION:
;    APPLICANT:  Suenaga, Masato
;    APPLICANT:  Moriya, Takeo
;    APPLICANT:  Tanaka, Yoko
;    APPLICANT:  Nishimura, Osamu
;    TITLE OF INVENTION:  METHOD OF PRODUCING A 19P2 LIGAND
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/105,678
;      FILING DATE:  26-JUN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 172118/1997
;      FILING DATE:  27-JUN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Conlin, David G.
;      REGISTRATION NUMBER:  27,026
;      REFERENCE/DOCKET NUMBER:  48466-342
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-105-678-31

  Query Match             100.0%;  Score 172;  DB 15;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-17;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 4
US-09-403-639A-39
; Sequence 39, Application US/09403639A
; GENERAL INFORMATION:
;  APPLICANT:  Hinuma, Shuji
;  APPLICANT:  Fukusumi, Shoji
;  TITLE OF INVENTION:  Polypeptides, their Production and Use
;  FILE REFERENCE:  2463US0P
;  CURRENT APPLICATION NUMBER: US/09/403,639A
;  CURRENT FILING DATE:  1998-04-27
;  PRIOR APPLICATION NUMBER:  PCT/JP98/01923
;  PRIOR FILING DATE:  1998-04-27
;  PRIOR APPLICATION NUMBER:  JP 9-109974
;  PRIOR FILING DATE:  1997-04-28
;  NUMBER OF SEQ ID NOS:  62
;  SOFTWARE:
; SEQ ID NO 39
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Bovine
US-09-403-639A-39

  Query Match             100.0%;  Score 172;  DB 18;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-17;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 5
US-09-403-639B-39
; Sequence 39, Application US/09403639B
```

```
; GENERAL INFORMATION:
;  APPLICANT: Hinuma, Shuji
;  APPLICANT:  Fukusumi, Shoji
;  TITLE OF INVENTION: Polypeptides, their Production and Use
;  FILE REFERENCE: 2463US0P
;  CURRENT APPLICATION NUMBER: US/09/403,639B
;  CURRENT FILING DATE:  1999-10-25
;  PRIOR APPLICATION NUMBER: PCT/JP98/01923
;  PRIOR FILING DATE: 1998-04-27
;  PRIOR APPLICATION NUMBER: JP 9-109974
;  PRIOR FILING DATE: 1997-04-28
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE:
; SEQ ID NO 39
;    LENGTH: 31
;    TYPE: PRT
;    ORGANISM: Bovine
US-09-403-639B-39

  Query Match             100.0%;  Score 172;  DB 18;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-17;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              ||||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 6
US-09-403-639C-39
; Sequence 39, Application US/09403639C
; GENERAL INFORMATION:
;  APPLICANT: Hinuma, Shuji
;  APPLICANT:  Fukusumi, Shoji
;  TITLE OF INVENTION: Polypeptides, their Production and Use
;  FILE REFERENCE: 2463US0P
;  CURRENT APPLICATION NUMBER: US/09/403,639C
;  CURRENT FILING DATE:  1999-10-25
;  PRIOR APPLICATION NUMBER: PCT/JP98/01923
;  PRIOR FILING DATE: 1998-04-27
;  PRIOR APPLICATION NUMBER: JP 9-109974
;  PRIOR FILING DATE: 1997-04-28
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE:
; SEQ ID NO 39
;    LENGTH: 31
;    TYPE: PRT
;    ORGANISM: Bovine
US-09-403-639C-39

  Query Match             100.0%;  Score 172;  DB 18;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-17;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              ||||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 7
US-09-446-543A-5
; Sequence 5, Application US/09446543A
; GENERAL INFORMATION:
;  APPLICANT:  HINUMA, Shuji
;  APPLICANT:  KAWAMATA, Yuji
;  APPLICANT:  FUJII, Ryo
;  APPLICANT:  MATSUMOTO, Hirokazu
;  TITLE OF INVENTION:  Prolactin Secretion Modulator
;  FILE REFERENCE:  2472US0P
;  CURRENT APPLICATION NUMBER: US/09/446,543A
;  CURRENT FILING DATE:  1999-12-20
;  PRIOR APPLICATION NUMBER:  PCT/JP98/02765
;  PRIOR FILING DATE:  1998-06-22
;  PRIOR APPLICATION NUMBER:  JP 9-165437
;  PRIOR FILING DATE:  1997-06-23
;  NUMBER OF SEQ ID NOS:  99
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 5
;    LENGTH: 31
;    TYPE: PRT
;    ORGANISM: artificial
;    FEATURE:
;    OTHER INFORMATION: bovine fragment (23-53)
US-09-446-543A-5

  Query Match             100.0%;  Score 172;  DB 18;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-17;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              ||||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 8
US-09-576-290-5
; Sequence 5, Application US/09576290
;  GENERAL INFORMATION:
;    APPLICANT:  Hinuma, Shuji
;    APPLICANT:  Habata, Yugo
;    APPLICANT:  Kawamata, Yuji
;    APPLICANT:  Hosoya, Masaki
;    APPLICANT:  Fujii, Ryo
;    APPLICANT:  Fukusumi, Shoji
;    APPLICANT:  Kitada, Chieko
;    TITLE OF INVENTION:  POLYPROTEINS, THEIR PRODUCTION AND USE
;    NUMBER OF SEQUENCES:  140
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/576,290
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/776,971
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7/343371
;      FILING DATE:  28-DEC-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 8/59419
;      FILING DATE:  15-MAR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 8/211805
;      FILING DATE:  12-AUG-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 8/246573
;      FILING DATE:  18-SEP-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Conlin, David G.
;      REGISTRATION NUMBER:  27,026
;      REFERENCE/DOCKET NUMBER:  47176
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;  INFORMATION FOR SEQ ID NO:  5:
```

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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-09-576-290-5

  Query Match             100.0%;  Score 172;  DB 19;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-17;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 9
US-09-576-290-97
; Sequence 97, Application US/09576290
; GENERAL INFORMATION:
;    APPLICANT:  Hinuma, Shuji
;    APPLICANT:  Habata, Yugo
;    APPLICANT:  Kawamata, Yuji
;    APPLICANT:  Hosoya, Masaki
;    APPLICANT:  Fujii, Ryo
;    APPLICANT:  Fukusumi, Shoji
;    APPLICANT:  Kitada, Chieko
;    TITLE OF INVENTION:  POLYPROTEINS, THEIR PRODUCTION AND USE
;    NUMBER OF SEQUENCES:  140
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/576,290
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/776,971
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7/343371
;      FILING DATE:  28-DEC-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 8/59419
;      FILING DATE:  15-MAR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 8/211805
;      FILING DATE:  12-AUG-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 8/246573
;      FILING DATE:  18-SEP-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Conlin, David G.
;      REGISTRATION NUMBER:  27,026
;      REFERENCE/DOCKET NUMBER:  47176
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;  INFORMATION FOR SEQ ID NO:  97:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-576-290-97

  Query Match             100.0%;  Score 172;  DB 19;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-17;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 10
US-09-716-147-5
; Sequence 5, Application US/09716147
;   GENERAL INFORMATION:
;        APPLICANT: Hinuma, Shuji
;                   Habata, Yugo
;                   Kawamata, Yuji
;                   Hosoya, Masaki
;                   Fujii, Ryo
;                   Fukusumi, Shoji
;                   Kitada, Chieko
;        TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
;        NUMBER OF SEQUENCES: 140
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;             STREET: 130 Water Street
;             CITY: Boston
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/716,147
;             FILING DATE: 17-Nov-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/776,971B
;             FILING DATE: 06-Feb-1997
;             APPLICATION NUMBER: PCT/JP96/03821
;             FILING DATE: 28-DEC-1996
;             APPLICATION NUMBER: JP 7/343371
;             FILING DATE: 28-DEC-1995
;             APPLICATION NUMBER: JP 8/59419
;             FILING DATE: 15-MAR-1996
;             APPLICATION NUMBER: JP 8/211805
;             FILING DATE: 12-AUG-1996
;             APPLICATION NUMBER: JP 8/246573
;             FILING DATE: 18-SEP-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Conlin, David G.
;             REGISTRATION NUMBER: 27,026
;             REFERENCE/DOCKET NUMBER: 47176
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 617-523-3400
;             TELEFAX: 617-523-6440
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 31 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        FRAGMENT TYPE: internal
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-716-147-5
```

```
  Query Match           100.0%;  Score 172;  DB 21;  Length 31;
  Best Local Similarity  100.0%;  Pred. No. 8.1e-17;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 11
US-09-716-147-97
; Sequence 97, Application US/09716147
;   GENERAL INFORMATION:
;        APPLICANT: Hinuma, Shuji
;                   Habata, Yugo
;                   Kawamata, Yuji
;                   Hosoya, Masaki
;                   Fujii, Ryo
;                   Fukusumi, Shoji
;                   Kitada, Chieko
;        TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
;        NUMBER OF SEQUENCES: 140
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;             STREET: 130 Water Street
;             CITY: Boston
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/716,147
;             FILING DATE: 17-Nov-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/776,971B
;             FILING DATE: 06-Feb-1997
;             APPLICATION NUMBER: PCT/JP96/03821
;             FILING DATE: 28-DEC-1996
;             APPLICATION NUMBER: JP 7/343371
;             FILING DATE: 28-DEC-1995
;             APPLICATION NUMBER: JP 8/59419
;             FILING DATE: 15-MAR-1996
;             APPLICATION NUMBER: JP 8/211805
;             FILING DATE: 12-AUG-1996
;             APPLICATION NUMBER: JP 8/246573
;             FILING DATE: 18-SEP-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Conlin, David G.
;             REGISTRATION NUMBER: 27,026
;             REFERENCE/DOCKET NUMBER: 47176
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 617-523-3400
;             TELEFAX: 617-523-6440
;   INFORMATION FOR SEQ ID NO: 97:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 31 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-09-716-147-97

  Query Match           100.0%;  Score 172;  DB 21;  Length 31;
  Best Local Similarity  100.0%;  Pred. No. 8.1e-17;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 12
US-09-868-885B-3
; Sequence 3, Application US/09868885B
; GENERAL INFORMATION:
;  APPLICANT: Takeda Chemical Industries, Ltd.
;  TITLE OF INVENTION: Use of Peptide
;  FILE REFERENCE: 2584WO0P
;  CURRENT APPLICATION NUMBER: US/09/868,885B
;  CURRENT FILING DATE:  2002-04-17
;  PRIOR APPLICATION NUMBER: JP 10-369585
;  PRIOR FILING DATE: 1998-12-25
;  NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 3
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Bovine
US-09-868-885B-3

  Query Match           100.0%;  Score 172;  DB 23;  Length 31;
  Best Local Similarity  100.0%;  Pred. No. 8.1e-17;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 13
US-09-932-161-13
; Sequence 13, Application US/09932161
; GENERAL INFORMATION:
;  APPLICANT: Civelli, Olivier
;  APPLICANT:  Lin, Steven
;  TITLE OF INVENTION: Screening and Therapeutic Methods For
;  TITLE OF INVENTION:  Promoting Wakefulness and Sleep
;  FILE REFERENCE: P-UC 4679
;  CURRENT APPLICATION NUMBER: US/09/932,161
;  CURRENT FILING DATE:  2001-08-17
;  PRIOR APPLICATION NUMBER: US 09/560,915
;  PRIOR FILING DATE: 2000-04-28
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Bos taurus
US-09-932-161-13

  Query Match           100.0%;  Score 172;  DB 24;  Length 31;
  Best Local Similarity  100.0%;  Pred. No. 8.1e-17;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31


RESULT 14
US-10-044-592-39
; Sequence 39, Application US/10044592
; GENERAL INFORMATION:
;  APPLICANT: Hinuma, Shuji
;  APPLICANT:  Fukusumi, Shoji
;  TITLE OF INVENTION: Polypeptides, their Production and Use
;  FILE REFERENCE: 2463US2P
;  CURRENT APPLICATION NUMBER: US/10/044,592
;  CURRENT FILING DATE:  2002-01-10
;  PRIOR APPLICATION NUMBER: US 09/403639
;  PRIOR FILING DATE: 1999-25-10
;  PRIOR APPLICATION NUMBER: PCT/JP98/01923
```

; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: JP 9-109974
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE:
; SEQ ID NO 39
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Bovine
US-10-044-592-39

Query Match 100.0%; Score 172; DB 26; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.1e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
Db 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 15
US-10-096-777-13
; Sequence 13, Application US/10096777
; GENERAL INFORMATION:
; APPLICANT: Civelli, Olivier
; APPLICANT: Lin, Steven
; TITLE OF INVENTION: Therapeutic Compositions and Methods
; TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)
; FILE REFERENCE: P-UC 3534
; CURRENT APPLICATION NUMBER: US/10/096,777
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US/09/560,915
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-096-777-13

Query Match 100.0%; Score 172; DB 26; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.1e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
Db 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

Search completed: November 12, 2003, 11:13:44
Job time : 173 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 12, 2003, 11:09:38 ; Search time 28 Seconds
(without alignments)
190.151 Million cell updates/sec

Title: US-09-446-543A-5
Perfect score: 172
Sequence: 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	172	100.0	31	9	US-09-932-161-13	Sequence 13, Appl
2	172	100.0	31	12	US-10-096-777-13	Sequence 13, Appl
3	172	100.0	31	14	US-10-044-592-39	Sequence 39, Appl
4	172	100.0	32	14	US-10-044-592-40	Sequence 40, Appl
5	172	100.0	33	14	US-10-044-592-41	Sequence 41, Appl
6	172	100.0	98	14	US-10-044-592-28	Sequence 28, Appl
7	172	100.0	98	14	US-10-044-592-38	Sequence 38, Appl
8	172	100.0	98	14	US-10-044-592-82	Sequence 82, Appl
9	172	100.0	98	14	US-10-044-592-84	Sequence 84, Appl
10	172	100.0	98	14	US-10-044-592-86	Sequence 86, Appl
11	172	100.0	98	14	US-10-044-592-88	Sequence 88, Appl
12	163	94.8	31	9	US-09-932-161-14	Sequence 14, Appl
13	163	94.8	31	12	US-10-096-777-14	Sequence 14, Appl
14	163	94.8	31	14	US-10-044-592-4	Sequence 4, Appli
15	163	94.8	31	14	US-10-044-592-5	Sequence 5, Appli
16	163	94.8	70	14	US-10-044-592-90	Sequence 90, Appl
17	163	94.8	82	14	US-10-044-592-1	Sequence 1, Appli
18	163	94.8	86	14	US-10-044-592-96	Sequence 96, Appl
19	163	94.8	91	14	US-10-044-592-94	Sequence 94, Appl
20	161	93.6	29	14	US-10-044-592-26	Sequence 26, Appl
21	158	91.9	31	9	US-09-932-161-15	Sequence 15, Appl
22	158	91.9	31	12	US-10-096-777-15	Sequence 15, Appl
23	158	91.9	87	14	US-10-044-592-92	Sequence 92, Appl
24	142	82.6	25	14	US-10-044-592-78	Sequence 78, Appl
25	115	66.9	20	9	US-09-932-161-16	Sequence 16, Appl
26	115	66.9	20	12	US-10-096-777-16	Sequence 16, Appl
27	115	66.9	20	14	US-10-044-592-42	Sequence 42, Appl
28	115	66.9	21	14	US-10-044-592-43	Sequence 43, Appl
29	115	66.9	22	14	US-10-044-592-44	Sequence 44, Appl
30	111	64.5	20	9	US-09-932-161-17	Sequence 17, Appl
31	111	64.5	20	12	US-10-096-777-17	Sequence 17, Appl
32	111	64.5	20	14	US-10-044-592-6	Sequence 6, Appli
33	109	63.4	19	14	US-10-044-592-27	Sequence 27, Appl
34	109	63.4	20	9	US-09-932-161-18	Sequence 18, Appl
35	109	63.4	20	12	US-10-096-777-18	Sequence 18, Appl
36	96	55.8	40	14	US-10-044-592-80	Sequence 80, Appl
37	61	35.5	428	9	US-09-820-155-2	Sequence 2, Appli
38	57	33.1	9	14	US-10-044-592-8	Sequence 8, Appli
39	57	33.1	465	12	US-10-301-822-197	Sequence 197, App
40	56	32.6	428	9	US-09-820-155-4	Sequence 4, Appli
41	54	31.4	10	14	US-10-044-592-9	Sequence 9, Appli
42	54	31.4	209	14	US-10-108-915-30	Sequence 30, Appl
43	52	30.2	417	10	US-09-738-626-4642	Sequence 4642, Ap
44	52	30.2	3594	10	US-09-911-842-4	Sequence 4, Appli
45	52	30.2	3594	14	US-10-150-821-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-932-161-13
; Sequence 13, Application US/09932161
; Patent No. US20020037533A1
; GENERAL INFORMATION:
; APPLICANT: Civelli, Olivier
; APPLICANT: Lin, Steven
; TITLE OF INVENTION: Screening and Therapeutic Methods For
; TITLE OF INVENTION: Promoting Wakefulness and Sleep
; FILE REFERENCE: P-UC 4679
; CURRENT APPLICATION NUMBER: US/09/932,161
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 09/560,915
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-932-161-13

Query Match 100.0%; Score 172; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 8e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
Db 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 2
US-10-096-777-13
; Sequence 13, Application US/10096777
; Publication No. US20030171270A1
; GENERAL INFORMATION:
; APPLICANT: Civelli, Olivier
; APPLICANT: Lin, Steven

; TITLE OF INVENTION: Therapeutic Compositions and Methods
; TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)
; FILE REFERENCE: P-UC 3534
; CURRENT APPLICATION NUMBER: US/10/096,777
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US/09/560,915
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-096-777-13

Query Match 100.0%; Score 172; DB 12; Length 31;
Best Local Similarity 100.0%; Pred. No. 8e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
Db 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 3
US-10-044-592-39
; Sequence 39, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Fukusumi, Shoji
; TITLE OF INVENTION: Polypeptides, their Production and Use
; FILE REFERENCE: 2463US2P
; CURRENT APPLICATION NUMBER: US/10/044,592
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIOR FILING DATE: 1999-25-10
; PRIOR APPLICATION NUMBER: PCT/JP98/01923
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: JP 9-109974
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE:
; SEQ ID NO 39
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Bovine
US-10-044-592-39

Query Match 100.0%; Score 172; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 8e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
Db 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 4
US-10-044-592-40
; Sequence 40, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Fukusumi, Shoji
; TITLE OF INVENTION: Polypeptides, their Production and Use
; FILE REFERENCE: 2463US2P
; CURRENT APPLICATION NUMBER: US/10/044,592
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIOR FILING DATE: 1999-25-10
; PRIOR APPLICATION NUMBER: PCT/JP98/01923
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: JP 9-109974
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE:
; SEQ ID NO 40
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Bovine
US-10-044-592-40

Query Match 100.0%; Score 172; DB 14; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.2e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
Db 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 5
US-10-044-592-41
; Sequence 41, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Fukusumi, Shoji
; TITLE OF INVENTION: Polypeptides, their Production and Use
; FILE REFERENCE: 2463US2P
; CURRENT APPLICATION NUMBER: US/10/044,592
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIOR FILING DATE: 1999-25-10
; PRIOR APPLICATION NUMBER: PCT/JP98/01923
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: JP 9-109974
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE:
; SEQ ID NO 41
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Bovine
US-10-044-592-41

Query Match 100.0%; Score 172; DB 14; Length 33;
Best Local Similarity 100.0%; Pred. No. 8.5e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
Db 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 6
US-10-044-592-28
; Sequence 28, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Fukusumi, Shoji
; TITLE OF INVENTION: Polypeptides, their Production and Use
; FILE REFERENCE: 2463US2P
; CURRENT APPLICATION NUMBER: US/10/044,592
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIOR FILING DATE: 1999-25-10
; PRIOR APPLICATION NUMBER: PCT/JP98/01923
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: JP 9-109974
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE:
; SEQ ID NO 28

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;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Murine
US-10-044-592-28

  Query Match           100.0%;  Score 172;  DB 14;  Length 98;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-17;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db         23 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 53


RESULT 7
US-10-044-592-38
; Sequence 38, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
;  APPLICANT: Hinuma, Shuji
;  APPLICANT:  Fukusumi, Shoji
;  TITLE OF INVENTION: Polypeptides, their Production and Use
;  FILE REFERENCE: 2463US2P
;  CURRENT APPLICATION NUMBER: US/10/044,592
;  CURRENT FILING DATE:  2002-01-10
;  PRIOR APPLICATION NUMBER: US 09/403639
;  PRIOR FILING DATE: 1999-25-10
;  PRIOR APPLICATION NUMBER: PCT/JP98/01923
;  PRIOR FILING DATE: 1998-04-27
;  PRIOR APPLICATION NUMBER: JP 9-109974
;  PRIOR FILING DATE: 1997-04-28
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE:
; SEQ ID NO 38
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Bovine
US-10-044-592-38

  Query Match           100.0%;  Score 172;  DB 14;  Length 98;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-17;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db         23 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 53


RESULT 8
US-10-044-592-82
; Sequence 82, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
;  APPLICANT: Hinuma, Shuji
;  APPLICANT:  Fukusumi, Shoji
;  TITLE OF INVENTION: Polypeptides, their Production and Use
;  FILE REFERENCE: 2463US2P
;  CURRENT APPLICATION NUMBER: US/10/044,592
;  CURRENT FILING DATE:  2002-01-10
;  PRIOR APPLICATION NUMBER: US 09/403639
;  PRIOR FILING DATE: 1999-25-10
;  PRIOR APPLICATION NUMBER: PCT/JP98/01923
;  PRIOR FILING DATE: 1998-04-27
;  PRIOR APPLICATION NUMBER: JP 9-109974
;  PRIOR FILING DATE: 1997-04-28
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE:
; SEQ ID NO 82
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Bovine
US-10-044-592-82

  Query Match           100.0%;  Score 172;  DB 14;  Length 98;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-17;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db         23 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 53


RESULT 9
US-10-044-592-84
; Sequence 84, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
;  APPLICANT: Hinuma, Shuji
;  APPLICANT:  Fukusumi, Shoji
;  TITLE OF INVENTION: Polypeptides, their Production and Use
;  FILE REFERENCE: 2463US2P
;  CURRENT APPLICATION NUMBER: US/10/044,592
;  CURRENT FILING DATE:  2002-01-10
;  PRIOR APPLICATION NUMBER: US 09/403639
;  PRIOR FILING DATE: 1999-25-10
;  PRIOR APPLICATION NUMBER: PCT/JP98/01923
;  PRIOR FILING DATE: 1998-04-27
;  PRIOR APPLICATION NUMBER: JP 9-109974
;  PRIOR FILING DATE: 1997-04-28
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE:
; SEQ ID NO 84
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Bovine
US-10-044-592-84

  Query Match           100.0%;  Score 172;  DB 14;  Length 98;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-17;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db         23 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 53


RESULT 10
US-10-044-592-86
; Sequence 86, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
;  APPLICANT: Hinuma, Shuji
;  APPLICANT:  Fukusumi, Shoji
;  TITLE OF INVENTION: Polypeptides, their Production and Use
;  FILE REFERENCE: 2463US2P
;  CURRENT APPLICATION NUMBER: US/10/044,592
;  CURRENT FILING DATE:  2002-01-10
;  PRIOR APPLICATION NUMBER: US 09/403639
;  PRIOR FILING DATE: 1999-25-10
;  PRIOR APPLICATION NUMBER: PCT/JP98/01923
;  PRIOR FILING DATE: 1998-04-27
;  PRIOR APPLICATION NUMBER: JP 9-109974
;  PRIOR FILING DATE: 1997-04-28
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE:
; SEQ ID NO 86
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Bovine
US-10-044-592-86

  Query Match           100.0%;  Score 172;  DB 14;  Length 98;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-17;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
```

```
Db         23 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 53


RESULT 11
US-10-044-592-88
; Sequence 88, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
;  APPLICANT: Hinuma, Shuji
;  APPLICANT:  Fukusumi, Shoji
;  TITLE OF INVENTION: Polypeptides, their Production and Use
;  FILE REFERENCE: 2463US2P
;  CURRENT APPLICATION NUMBER: US/10/044,592
;  CURRENT FILING DATE:  2002-01-10
;  PRIOR APPLICATION NUMBER: US 09/403639
;  PRIOR FILING DATE: 1999-25-10
;  PRIOR APPLICATION NUMBER: PCT/JP98/01923
;  PRIOR FILING DATE: 1998-04-27
;  PRIOR APPLICATION NUMBER: JP 9-109974
;  PRIOR FILING DATE: 1997-04-28
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE:
; SEQ ID NO 88
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Bovine
US-10-044-592-88

  Query Match             100.0%;  Score 172;  DB 14;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-17;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||||||||||||||||||||||||||
Db         23 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 53


RESULT 12
US-09-932-161-14
; Sequence 14, Application US/09932161
; Patent No. US20020037533A1
; GENERAL INFORMATION:
;  APPLICANT: Civelli, Olivier
;  APPLICANT:  Lin, Steven
;  TITLE OF INVENTION: Screening and Therapeutic Methods For
;  TITLE OF INVENTION:  Promoting Wakefulness and Sleep
;  FILE REFERENCE: P-UC 4679
;  CURRENT APPLICATION NUMBER: US/09/932,161
;  CURRENT FILING DATE:  2001-08-17
;  PRIOR APPLICATION NUMBER: US 09/560,915
;  PRIOR FILING DATE: 2000-04-28
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Rattus
US-09-932-161-14

  Query Match             94.8%;  Score 163;  DB 9;  Length 31;
  Best Local Similarity   93.5%;  Pred. No. 1.6e-16;
  Matches   29;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              ||||||||| |||||||||| ||||||||||
Db          1 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31


RESULT 13
US-10-096-777-14
; Sequence 14, Application US/10096777
; Publication No. US20030171270A1
; GENERAL INFORMATION:
;  APPLICANT: Civelli, Olivier
;  APPLICANT:  Lin, Steven
;  TITLE OF INVENTION: Therapeutic Compositions and Methods
;  TITLE OF INVENTION:  Relating To Prolactin Releasing Peptide (PrRP)
;  FILE REFERENCE: P-UC 3534
;  CURRENT APPLICATION NUMBER: US/10/096,777
;  CURRENT FILING DATE:  2002-03-12
;  PRIOR APPLICATION NUMBER: US/09/560,915
;  PRIOR FILING DATE: 2000-04-28
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Rattus
US-10-096-777-14

  Query Match             94.8%;  Score 163;  DB 12;  Length 31;
  Best Local Similarity   93.5%;  Pred. No. 1.6e-16;
  Matches   29;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              ||||||||| |||||||||| ||||||||||
Db          1 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31


RESULT 14
US-10-044-592-4
; Sequence 4, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
;  APPLICANT: Hinuma, Shuji
;  APPLICANT:  Fukusumi, Shoji
;  TITLE OF INVENTION: Polypeptides, their Production and Use
;  FILE REFERENCE: 2463US2P
;  CURRENT APPLICATION NUMBER: US/10/044,592
;  CURRENT FILING DATE:  2002-01-10
;  PRIOR APPLICATION NUMBER: US 09/403639
;  PRIOR FILING DATE: 1999-25-10
;  PRIOR APPLICATION NUMBER: PCT/JP98/01923
;  PRIOR FILING DATE: 1998-04-27
;  PRIOR APPLICATION NUMBER: JP 9-109974
;  PRIOR FILING DATE: 1997-04-28
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE:
; SEQ ID NO 4
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Murine
US-10-044-592-4

  Query Match             94.8%;  Score 163;  DB 14;  Length 31;
  Best Local Similarity   93.5%;  Pred. No. 1.6e-16;
  Matches   29;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              ||||||||| |||||||||| ||||||||||
Db          1 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31


RESULT 15
US-10-044-592-5
; Sequence 5, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
;  APPLICANT: Hinuma, Shuji
;  APPLICANT:  Fukusumi, Shoji
;  TITLE OF INVENTION: Polypeptides, their Production and Use
;  FILE REFERENCE: 2463US2P
;  CURRENT APPLICATION NUMBER: US/10/044,592
;  CURRENT FILING DATE:  2002-01-10
;  PRIOR APPLICATION NUMBER: US 09/403639
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; PRIOR FILING DATE: 1999-25-10
; PRIOR APPLICATION NUMBER: PCT/JP98/01923
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: JP 9-109974
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE:
; SEQ ID NO 5
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(31)
; OTHER INFORMATION: antigen
US-10-044-592-5

Query Match 94.8%; Score 163; DB 14; Length 31;
Best Local Similarity 93.5%; Pred. No. 1.6e-16;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |:|||||||| |:|||||:||| |||:|||||||
Db          1 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31
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Search completed: November 12, 2003, 11:14:55
Job time : 28 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 12, 2003, 11:08:48 ; Search time 18 Seconds
(without alignments)
82.426 Million cell updates/sec

Title: US-09-446-543A-5
Perfect score: 172
Sequence: 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 252157 seqs, 47860546 residues

Total number of hits satisfying chosen parameters: 252157

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
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7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	57	33.1	492	7	US-60-478-196-3124	Sequence 3124, Ap
2	51.5	29.9	664	6	US-10-389-647-469	Sequence 469, App
3	48.5	28.2	380	1	PCT-US03-30292-394	Sequence 394, App
4	48.5	28.2	380	1	PCT-US03-30292-1500	Sequence 1500, Ap
5	48.5	28.2	380	6	US-10-666-642-394	Sequence 394, App
6	48.5	28.2	380	6	US-10-666-642-1500	Sequence 1500, Ap
7	48.5	28.2	1091	6	US-10-679-063-8843	Sequence 8843, Ap
8	48	27.9	117	5	US-09-979-932A-611	Sequence 611, App
9	48	27.9	190	6	US-10-679-063-5285	Sequence 5285, Ap
10	48	27.9	234	6	US-10-425-114A-62112	Sequence 62112, A
11	48	27.9	293	6	US-10-679-063-10848	Sequence 10848, A
12	48	27.9	314	6	US-10-679-063-10224	Sequence 10224, A
13	48	27.9	525	6	US-10-425-114A-51299	Sequence 51299, A
14	48	27.9	535	6	US-10-425-114A-60539	Sequence 60539, A
15	48	27.9	541	6	US-10-425-114A-50166	Sequence 50166, A
16	48	27.9	591	6	US-10-425-114A-50253	Sequence 50253, A
17	48	27.9	637	6	US-10-679-063-11393	Sequence 11393, A
18	48	27.9	746	6	US-10-425-114A-64563	Sequence 64563, A
19	48	27.9	746	6	US-10-425-114A-68107	Sequence 68107, A
20	47	27.3	345	5	US-09-976-858-171	Sequence 171, App
21	47	27.3	455	6	US-10-679-063-10212	Sequence 10212, A
22	47	27.3	455	6	US-10-679-063-10845	Sequence 10845, A
23	46.5	27.0	337	6	US-10-296-115-1208	Sequence 1208, Ap
24	46.5	27.0	770	6	US-10-679-063-9397	Sequence 9397, Ap
25	46.5	27.0	770	6	US-10-679-063-12917	Sequence 12917, A
26	46.5	27.0	770	6	US-10-679-063-13708	Sequence 13708, A
27	46.5	27.0	770	6	US-10-679-063-23837	Sequence 23837, A
28	46.5	27.0	843	5	US-09-581-286A-432	Sequence 432, App
29	46.5	27.0	849	5	US-09-581-286A-307	Sequence 307, App
30	46	26.7	316	6	US-10-425-114A-57023	Sequence 57023, A
31	46	26.7	633	6	US-10-425-114A-56709	Sequence 56709, A
32	46	26.7	774	6	US-10-408-601-30	Sequence 30, Appl
33	46	26.7	943	1	PCT-US03-10309A-26	Sequence 26, Appl
34	46	26.7	943	6	US-10-406-686A-26	Sequence 26, Appl
35	46	26.7	1420	7	US-60-478-196-3131	Sequence 3131, Ap
36	45	26.2	91	1	PCT-US03-31535-3	Sequence 3, Appli
37	45	26.2	178	6	US-10-472-928-266	Sequence 266, App
38	45	26.2	367	6	US-10-679-063-13181	Sequence 13181, A
39	45	26.2	367	6	US-10-679-063-15278	Sequence 15278, A
40	45	26.2	404	5	US-09-897-516A-5041	Sequence 5041, Ap
41	45	26.2	940	5	US-09-581-286A-463	Sequence 463, App
42	45	26.2	943	5	US-09-897-516A-6220	Sequence 6220, Ap
43	45	26.2	962	5	US-09-581-286A-336	Sequence 336, App
44	44.5	25.9	131	6	US-10-425-114A-48795	Sequence 48795, A
45	44.5	25.9	152	7	US-60-490-890-1908	Sequence 1908, Ap

ALIGNMENTS

RESULT 1
US-60-478-196-3124
; Sequence 3124, Application US/60478196
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Lemieux, Sebastien
; APPLICANT: Hu, Wenqi
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF ASPERGILLUS FUMIGATUS AND
; TITLE OF INVENTION: USE
; FILE REFERENCE: 10182-026-888
; CURRENT APPLICATION NUMBER: US/60/478,196
; CURRENT FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 4000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3124
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-60-478-196-3124

Query Match 33.1%; Score 57; DB 7; Length 492;
Best Local Similarity 43.5%; Pred. No. 9.2;
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

```
Qy          3 AHQHSMEIRTPDINPAWYAGRGI 25
              :| |.::   |:|: || ||  |
Db        248 SHAHGVQALGPNINAAWLAGGSI 270
```

RESULT 2
US-10-389-647-469
; Sequence 469, Application US/10389647
; GENERAL INFORMATION:
; APPLICANT: GREENBERG, E. Peter
; APPLICANT: SCHUSTER, Martin
; APPLICANT: LOSTROH, Candi
; TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA
; FILE REFERENCE: UIZ-038CP
; CURRENT APPLICATION NUMBER: US/10/389,647
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 09/653730
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/153022
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 710
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 469
; LENGTH: 664

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;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-10-389-647-469

  Query Match             29.9%;  Score 51.5;  DB 6;  Length 664;
  Best Local Similarity   55.6%;  Pred. No. 52;
  Matches   10;  Conservative    2;  Mismatches    5;  Indels    1;  Gaps    1;

Qy         10 IRTPDINPAWYAGRGIRP 27
              : |||||| |:  |  ||
Db        476 VNTPDINP-WFLQRSGRP 492


RESULT 3
PCT-US03-30292-394
; Sequence 394, Application PC/TUS0330292
; GENERAL INFORMATION:
;  APPLICANT: Mendel Biotechnology, Inc.
;  APPLICANT:  JIANG, Cai-Zhong
;  APPLICANT:  HEARD, Jacqueline E
;  APPLICANT:  RATCLIFFE, Oliver
;  APPLICANT:  CREELMAN, Robert A
;  APPLICANT:  ADAM, Luc J
;  APPLICANT:  REUBER, T. Lynne
;  APPLICANT:  RIECHMANN, Jose Luis
;  APPLICANT:  HAAKE, Volker
;  APPLICANT:  DUBELL, Arnold N
;  APPLICANT:  KEDDIE, James S
;  APPLICANT:  SHERMAN, Bradley K
;  TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
;  FILE REFERENCE: MBI-0054
;  CURRENT APPLICATION NUMBER: PCT/US03/30292
;  CURRENT FILING DATE:  2003-09-22
;  PRIOR APPLICATION NUMBER: 60/411,837
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/434,166
;  PRIOR FILING DATE: 2002-12-17
;  PRIOR APPLICATION NUMBER: 60/465,809
;  PRIOR FILING DATE: 2003-04-24
;  NUMBER OF SEQ ID NOS: 2247
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 394
;   LENGTH: 380
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
PCT-US03-30292-394

  Query Match             28.2%;  Score 48.5;  DB 1;  Length 380;
  Best Local Similarity   35.5%;  Pred. No. 80;
  Matches   11;  Conservative    3;  Mismatches   10;  Indels    7;  Gaps    1;

Qy          1 SRAHQ-------HSMEIRTPDINPAWYAGRG 24
              |  ;|       ; ::   |   |:|| |||
Db        118 SLLHQSPMHFLHHPLQHSFPHHQPSWYWGRG 148


RESULT 4
PCT-US03-30292-1500
; Sequence 1500, Application PC/TUS0330292
; GENERAL INFORMATION:
;  APPLICANT: Mendel Biotechnology, Inc.
;  APPLICANT:  JIANG, Cai-Zhong
;  APPLICANT:  HEARD, Jacqueline E
;  APPLICANT:  RATCLIFFE, Oliver
;  APPLICANT:  CREELMAN, Robert A
;  APPLICANT:  ADAM, Luc J
;  APPLICANT:  REUBER, T. Lynne
;  APPLICANT:  RIECHMANN, Jose Luis
;  APPLICANT:  HAAKE, Volker
;  APPLICANT:  DUBELL, Arnold N
;  APPLICANT:  KEDDIE, James S
;  APPLICANT:  SHERMAN, Bradley K
;  TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
;  FILE REFERENCE: MBI-0054
;  CURRENT APPLICATION NUMBER: PCT/US03/30292
;  CURRENT FILING DATE:  2003-09-22
;  PRIOR APPLICATION NUMBER: 60/411,837
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/434,166
;  PRIOR FILING DATE: 2002-12-17
;  PRIOR APPLICATION NUMBER: 60/465,809
;  PRIOR FILING DATE: 2003-04-24
;  NUMBER OF SEQ ID NOS: 2247
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1500
;   LENGTH: 380
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
PCT-US03-30292-1500

  Query Match             28.2%;  Score 48.5;  DB 1;  Length 380;
  Best Local Similarity   35.5%;  Pred. No. 80;
  Matches   11;  Conservative    3;  Mismatches   10;  Indels    7;  Gaps    1;

Qy          1 SRAHQ-------HSMEIRTPDINPAWYAGRG 24
              |  ||       | ::   |   |:|| |||
Db        118 SLLHQSPMHFLHHPLQHSFPHHQPSWYWGRG 148


RESULT 5
US-10-666-642-394
; Sequence 394, Application US/10666642
; GENERAL INFORMATION:
;  APPLICANT: Mendel Biotechnology, Inc.
;  APPLICANT:  JIANG, Cai-Zhong
;  APPLICANT:  HEARD, Jacqueline E
;  APPLICANT:  RATCLIFFE, Oliver
;  APPLICANT:  CREELMAN, Robert A
;  APPLICANT:  ADAM, Luc J
;  APPLICANT:  REUBER, T. Lynne
;  APPLICANT:  RIECHMANN, Jose Luis
;  APPLICANT:  HAAKE, Volker
;  APPLICANT:  DUBELL, Arnold N
;  APPLICANT:  KEDDIE, James S
;  APPLICANT:  SHERMAN, Bradley K
;  TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
;  FILE REFERENCE: MBI-0054
;  CURRENT APPLICATION NUMBER: US/10/666,642
;  CURRENT FILING DATE:  2003-09-18
;  PRIOR APPLICATION NUMBER: 60/411,837
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/434,166
;  PRIOR FILING DATE: 2002-12-17
;  PRIOR APPLICATION NUMBER: 60/465,809
;  PRIOR FILING DATE: 2003-04-24
;  NUMBER OF SEQ ID NOS: 2247
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 394
;   LENGTH: 380
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-10-666-642-394

  Query Match             28.2%;  Score 48.5;  DB 6;  Length 380;
  Best Local Similarity   35.5%;  Pred. No. 80;
  Matches   11;  Conservative    3;  Mismatches   10;  Indels    7;  Gaps    1;

Qy          1 SRAHQ-------HSMEIRTPDINPAWYAGRG 24
              |  ||       | ::   |   |:|| |||
Db        118 SLLHQSPMHFLHHPLQHSFPHHQPSWYWGRG 148


RESULT 6
US-10-666-642-1500
; Sequence 1500, Application US/10666642
; GENERAL INFORMATION:
```

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;  APPLICANT: Mendel Biotechnology, Inc.
;  APPLICANT:  JIANG, Cai-Zhong
;  APPLICANT:  HEARD, Jacqueline E
;  APPLICANT:  RATCLIFFE, Oliver
;  APPLICANT:  CREELMAN, Robert A
;  APPLICANT:  ADAM, Luc J
;  APPLICANT:  REUBER, T. Lynne
;  APPLICANT:  RIECHMANN, Jose Luis
;  APPLICANT:  HAAKE, Volker
;  APPLICANT:  DUBELL, Arnold N
;  APPLICANT:  KEDDIE, James S
;  APPLICANT:  SHERMAN, Bradley K
;  TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
;  FILE REFERENCE: MBI-0054
;  CURRENT APPLICATION NUMBER: US/10/666,642
;  CURRENT FILING DATE:  2003-09-18
;  PRIOR APPLICATION NUMBER: 60/411,837
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: 60/434,166
;  PRIOR FILING DATE: 2002-12-17
;  PRIOR APPLICATION NUMBER: 60/465,809
;  PRIOR FILING DATE: 2003-04-24
;  NUMBER OF SEQ ID NOS: 2247
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1500
;   LENGTH: 380
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-10-666-642-1500

  Query Match             28.2%;  Score 48.5;  DB 6;  Length 380;
  Best Local Similarity   35.5%;  Pred. No. 80;
  Matches   11;  Conservative    3;  Mismatches   10;  Indels    7;  Gaps    1;

Qy          1 SRAHQ-------HSMEIRTPDINPAWYAGRG 24
                 ||       | ::   |   |:|| |||
Db        118 SLLHQSPMHFLHHPLQHSFPHHQPSWYWGRG 148


RESULT 7
US-10-679-063-8843
; Sequence 8843, Application US/10679063
; GENERAL INFORMATION:
;  APPLICANT: Edgerton, Michael D
;  TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
;  FILE REFERENCE: 38-15(52054)B
;  CURRENT APPLICATION NUMBER: US/10/679,063
;  CURRENT FILING DATE:  2003-10-02
;  PRIOR APPLICATION NUMBER: 60/415,758
;  PRIOR FILING DATE: 2002-10-02
;  NUMBER OF SEQ ID NOS: 27373
; SEQ ID NO 8843
;   LENGTH: 1091
;   TYPE: PRT
;   ORGANISM: Nicotiana alata
US-10-679-063-8843

  Query Match             28.2%;  Score 48.5;  DB 6;  Length 1091;
  Best Local Similarity   37.8%;  Pred. No. 1.7e+02;
  Matches   14;  Conservative    4;  Mismatches   12;  Indels    7;  Gaps    2;

Qy          2 RAHQ------HSMEIRTPDINPAWYA-GRGIRPVGRF 31
              | ||       |:||      | ||  | |::|: ||
Db        827 RLHQVLRWALGSVEILLSKHCPIWYGYGCGLKPLERF 863


RESULT 8
US-09-979-932A-611
; Sequence 611, Application US/09979932A
; GENERAL INFORMATION:
;  APPLICANT: Obata, Yuichi
;  TITLE OF INVENTION: BREAST, GASTRIC, AND PROSTATE CANCER ASSOCIATED ANTIGENS AND
;  TITLE OF INVENTION:  USES THEREFOR
;  FILE REFERENCE: L00461.70122.US
;  CURRENT APPLICATION NUMBER: US/09/979,932A
;  CURRENT FILING DATE:  2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/136,526
;  PRIOR FILING DATE: 1999-05-28
;  PRIOR APPLICATION NUMBER: US 60/153,454
;  PRIOR FILING DATE: 1999-09-10
;  NUMBER OF SEQ ID NOS: 1332
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 611
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-979-932A-611

  Query Match             27.9%;  Score 48;  DB 5;  Length 117;
  Best Local Similarity   57.9%;  Pred. No. 39;
  Matches   11;  Conservative    2;  Mismatches    4;  Indels    2;  Gaps    1;

Qy         11 RTPDINP--AWYAGRGIRP 27
                 ||    :|  ||:|'|| ||
Db          9 RTGTRSPMEAWHAGRGNRP 27


RESULT 9
US-10-679-063-5285
; Sequence 5285, Application US/10679063
; GENERAL INFORMATION:
;  APPLICANT: Edgerton, Michael D
;  TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
;  FILE REFERENCE: 38-15(52054)B
;  CURRENT APPLICATION NUMBER: US/10/679,063
;  CURRENT FILING DATE:  2003-10-02
;  PRIOR APPLICATION NUMBER: 60/415,758
;  PRIOR FILING DATE: 2002-10-02
;  NUMBER OF SEQ ID NOS: 27373
; SEQ ID NO 5285
;   LENGTH: 190
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(190)
;   OTHER INFORMATION: unsure at all Xaa locations
US-10-679-063-5285

  Query Match             27.9%;  Score 48;  DB 6;  Length 190;
  Best Local Similarity   48.0%;  Pred. No. 55;
  Matches   12;  Conservative    2;  Mismatches    7;  Indels    4;  Gaps    1;

Qy          4 HQHSMEIR----TPDINPAWYAGRG 24
              | |:|||      ||     :|||||
Db        163 HDKSIEIRKYSSLPDRPTMFYAGRG 187


RESULT 10
US-10-425-114A-62112
; Sequence 62112, Application US/10425114A
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114A
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 62112
;   LENGTH: 234
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;   TYPE: PRT
;   ORGANISM: Gossypium hirsutum
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB3166-014-B6_FLI.pep
US-10-425-114A-62112

  Query Match             27.9%;  Score 48;  DB 6;  Length 234;
  Best Local Similarity   33.3%;  Pred. No. 64;
  Matches    9;  Conservative    5;  Mismatches    7;  Indels    6;  Gaps    1;

Qy          8 MEIRTPDINPAWYAG------RGIRPV 28
              :: ||  :|| || |      |:| :
Db        119 LDARTKLLNPKWYEGMMSSGYEGVREI 145


RESULT 11
US-10-679-063-10848
; Sequence 10848, Application US/10679063
; GENERAL INFORMATION:
;  APPLICANT: Edgerton, Michael D
;  TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
;  FILE REFERENCE: 38-15(52054)B
;  CURRENT APPLICATION NUMBER: US/10/679,063
;  CURRENT FILING DATE:  2003-10-02
;  PRIOR APPLICATION NUMBER: 60/415,758
;  PRIOR FILING DATE: 2002-10-02
;  NUMBER OF SEQ ID NOS: 27373
; SEQ ID NO 10848
;   LENGTH: 293
;   TYPE: PRT
;   ORGANISM: Mycobacterium tuberculosis CDC1551
US-10-679-063-10848

  Query Match             27.9%;  Score 48;  DB 6;  Length 293;
  Best Local Similarity   32.0%;  Pred. No. 76;
  Matches    8;  Conservative    5;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          3 AHQHSMEIRTPDINPAWYAGRGIRP 27
              |  | |::   :: |:|     |||
Db        181 AVDHMMKLAADELGPSWVRVNSIRP 205


RESULT 12
US-10-679-063-10224
; Sequence 10224, Application US/10679063
; GENERAL INFORMATION:
;  APPLICANT: Edgerton, Michael D
;  TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
;  FILE REFERENCE: 38-15(52054)B
;  CURRENT APPLICATION NUMBER: US/10/679,063
;  CURRENT FILING DATE:  2003-10-02
;  PRIOR APPLICATION NUMBER: 60/415,758
;  PRIOR FILING DATE: 2002-10-02
;  NUMBER OF SEQ ID NOS: 27373
; SEQ ID NO 10224
;   LENGTH: 314
;   TYPE: PRT
;   ORGANISM: Mycobacterium tuberculosis H37Rv
US-10-679-063-10224

  Query Match             27.9%;  Score 48;  DB 6;  Length 314;
  Best Local Similarity   32.0%;  Pred. No. 80;
  Matches    8;  Conservative    5;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          3 AHQHSMEIRTPDINPAWYAGRGIRP 27
              |  | |::   :: |:|     |||
Db        202 AVDHMMKLAADELGPSWVRVNSIRP 226


RESULT 13
US-10-425-114A-51299
; Sequence 51299, Application US/10425114A
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114A
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 51299
;   LENGTH: 525
;   TYPE: PRT
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 700045010_FLI.pep
US-10-425-114A-51299

  Query Match             27.9%;  Score 48;  DB 6;  Length 525;
  Best Local Similarity   33.3%;  Pred. No. 1.2e+02;
  Matches    9;  Conservative    5;  Mismatches    7;  Indels    6;  Gaps    1;

Qy          8 MEIRTPDINPAWYAG------RGIRPV 28
              :: ||  :|| || |      |:| :
Db        410 LDARTKLLNPKWYEGMMKSGYEGVREI 436


RESULT 14
US-10-425-114A-60539
; Sequence 60539, Application US/10425114A
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114A
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 60539
;   LENGTH: 535
;   TYPE: PRT
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: UC-ZMFLM017286A02_FLI.pep
US-10-425-114A-60539

  Query Match             27.9%;  Score 48;  DB 6;  Length 535;
  Best Local Similarity   35.0%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    6;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         10 IRTPDINPAWYAGRGIRPVG 29
              :||  ::| |:: ||:   |
Db        143 LRTDPVSPTWHSTRGVSEDG 162


RESULT 15
US-10-425-114A-50166
; Sequence 50166, Application US/10425114A
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
```

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;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114A
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 50166
;   LENGTH: 541
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 700890310_FLI.pep
US-10-425-114A-50166

  Query Match             27.9%;  Score 48;  DB 6;  Length 541;
  Best Local Similarity   33.3%;  Pred. No. 1.2e+02;
  Matches    9;  Conservative    5;  Mismatches    7;  Indels    6;  Gaps    1;

Qy          8 MEIRTPDINPAWYAG------RGIRPV 28
              :: !!  :|| '| |      ':| :
Db        426 LDARTKLLNPKWYEGMLSTGYEGVREI 452


Search completed: November 12, 2003, 11:14:14
Job time : 18 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 12, 2003, 11:06:47 ; Search time 21 Seconds
(without alignments)
141.963 Million cell updates/sec

Title: US-09-446-543A-5
Perfect score: 172
Sequence: 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	163	94.8	83	2	JC7607	prolactin-releasin
2	56.5	32.8	303	2	AH2016	hypothetical prote
3	55	32.0	1236	2	T50904	Mg protoporphyrin
4	54.5	31.7	503	2	A82193	Sun/nucleolar prot
5	53.5	31.1	176	2	S67150	hypothetical prote
6	53	30.8	376	2	C75580	adenine deaminase-
7	52	30.2	73	2	A98137	hypothetical prote
8	52	30.2	308	2	AH2896	transcription regu
9	52	30.2	308	2	B97672	rok family protein
10	52	30.2	419	2	AH3166	hypothetical prote
11	52	30.2	1292	2	T31462	probable magnesium
12	51.5	29.9	664	2	F83376	conserved hypothet
13	51	29.7	294	2	T21075	hypothetical prote
14	51	29.7	430	1	B69009	conserved hypothet
15	51	29.7	798	2	S11210	probable unr prote
16	51	29.7	962	2	H69157	excinuclease ABC c
17	50.5	29.4	790	2	T47959	hypothetical prote
18	50	29.1	527	2	T33175	hypothetical prote
19	50	29.1	974	2	AH3361	excinuclease ABC c
20	49.5	28.8	393	2	AB2664	conserved hypothet
21	49.5	28.8	401	2	A97446	hypothetical prote
22	49	28.5	128	2	S76955	hypothetical prote
23	49	28.5	226	2	A87664	hypothetical prote
24	48.5	28.2	254	2	S76814	hypothetical prote
25	48.5	28.2	548	2	T47548	hypothetical prote
26	48.5	28.2	1882	2	S73484	hypothetical prote
27	48	27.9	72	2	E91002	probable regulator
28	48	27.9	220	2	C83292	probable glutathio
29	48	27.9	314	2	B70569	hypothetical prote
30	48	27.9	348	2	T21648	hypothetical prote
31	48	27.9	365	2	T39098	hypothetical prote
32	48	27.9	397	2	JC7675	acetoacetyl-CoA re
33	48	27.9	424	2	B38176	samB protein - Sal
34	48	27.9	637	2	D87559	sensory box histid
35	48	27.9	772	2	T07958	protoporphyrin IX
36	48	27.9	960	2	A71315	excinuclease ABC c
37	48	27.9	973	2	AH2762	ABC excinuclease s
38	48	27.9	982	2	G97543	excinuclease ABC c
39	48	27.9	1328	2	AE2351	protoporphyrin IX
40	48	27.9	1331	2	S75000	protoporphyrin IX
41	48	27.9	1379	2	S37310	protoporphyrin IX
42	48	27.9	1380	2	S64721	protoporphyrin IX
43	48	27.9	1381	2	S71288	protoporphyrin IX
44	48	27.9	1382	2	T01789	protoporphyrin IX
45	48	27.9	1383	2	T07126	magnesium chelatas

ALIGNMENTS

RESULT 1
JC7607
prolactin-releasing peptide - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C;Accession: JC7607
R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, Biochem. Biophys. Res. Commun. 281, 53-56, 2001
A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene:
A;Reference number: JC7607; MUID:21092785; PMID:11178959
A;Contents: Spleen
A;Accession: JC7607
A;Molecule type: DNA
A;Residues: 1-83 <YAM>
A;Cross-references: DDBJ:AB040612; DDBJ:AB040613
C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary.
C;Genetics:
A;Gene: PrRP
A;Introns: 33/1

Query Match 94.8%; Score 163; DB 2; Length 83;
Best Local Similarity 93.5%; Pred. No. 6.9e-17;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |||||||| |||||||||| |||||||||||
Db         22 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 52
```

RESULT 2
AH2016
hypothetical protein all1686 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AH2016
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH2016
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-303 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB78052.1; PID:g17135506; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all1686

Query Match 32.8%; Score 56.5; DB 2; Length 303;

```
  Best Local Similarity   51.6%;  Pred. No. 1.5;
  Matches   16;  Conservative    2;  Mismatches    8;  Indels    5;  Gaps    2;

Qy          4 HQHSMEIRTPDINPAWY----AGRGIRPVGR 30
              |:|| | ||  |:   |    || | ||||| |
Db        226 HEHSYE-RTRAIDGTTYLTCGAGAGNRPVGR 255


RESULT 3
T50904
Mg protoporphyrin methyl transferase [imported] - Rubrivivax gelatinosus
C;Species: Rubrivivax gelatinosus
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
C;Accession: T50904
R;Nagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K.
submitted to the EMBL Data Library, November 1999
A;Description: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photosynt
A;Reference number: Z25270
A;Accession: T50904
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1236 <NAG>
A;Cross-references: EMBL:AB034704; PIDN:BAA94057.1
A;Experimental source: strain IL144
C;Genetics:
A;Gene: bchH
C;Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase

  Query Match             32.0%;  Score 55;  DB 2;  Length 1236;
  Best Local Similarity   34.4%;  Pred. No. 11;
  Matches   11;  Conservative    6;  Mismatches    9;  Indels    6;  Gaps    1;

Qy          3 AHQHSMEIRTPDINPAWYAG------RGIRPV 28
              : | ::| |'  :|| || |       |:| :
Db       1112 SEQVALETRTRMLNPKWYEGMLEHGYEGVRQI 1143


RESULT 4
A82193
Sun/nucleolar protein family protein VC1502 [imported] - Vibrio cholerae (strain N16961
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: A82193
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
l, R.R.; Mekalanos, J.C.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: A82193
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-503 <HEI>
A;Cross-references: GB:AE004228; GB:AE003852; NID:g9655997; PIDN:AAF94657.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC1502
A;Map position: 1

  Query Match             31.7%;  Score 54.5;  DB 2;  Length 503;
  Best Local Similarity   36.7%;  Pred. No. 5;
  Matches   11;  Conservative    6;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
              | :  ||:|: |      |: || :|| |:
Db        435 SSSASHSVELDTTQAR-EWFMGRDVRPEGQ 463


RESULT 5
S67150
hypothetical protein YOR253w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O5315
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C;Accession: S67150
R;Jauniaux, J.C.; Poirey, R.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67143
A;Accession: S67150
A;Molecule type: DNA
A;Residues: 1-176 <JAU>
A;Cross-references: EMBL:Z75161; NID:g1420572; PID:e252411; PID:g1420573; GSPDB:GN000
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YOR253w
A;Cross-references: SGD:S0005779
A;Map position: 15R

  Query Match             31.1%;  Score 53.5;  DB 2;  Length 176;
  Best Local Similarity   31.2%;  Pred. No. 2.3;
  Matches   10;  Conservative    5;  Mismatches   14;  Indels    3;  Gaps    1;

Qy          1 SRAHQHSMEIRTP---DINPAWYAGRGIRPVG 29
              |  |||:: :  !   |:   |:  |   .|
Db        120 SECHQHNVFVYLPAVDDLTKQWFIAHGFEQVG 151


RESULT 6
C75580
adenine deaminase-related protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: C75580
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: C75580
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <WHI>
A;Cross-references: GB:AE001863; GB:AE001925; NID:g6460670; PIDN:AAF12376.1; PID:g646
A;Experimental source: strain R1
C;Genetics:
A;Gene: DRA0268
A;Map position: 2

  Query Match             30.8%;  Score 53;  DB 2;  Length 376;
  Best Local Similarity   40.0%;  Pred. No. 6.1;
  Matches   12;  Conservative    6;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
              :||  |: ::  || : |  ||:  |: ||
Db        177 ARALAHAPDVSRPDRHRACGAGQRRRPAGR 206


RESULT 7
A98137
hypothetical protein AGR_L_109 [imported] - Agrobacterium tumefaciens (strain C58, Ce
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: A98137
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: A98137
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-73 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK88619.1; PID:g15158338; GSPDB:GN00170
C;Genetics:
A;Gene: AGR_L_109
```

A;Map position: linear chromosome

Query Match 30.2%; Score 52; DB 2; Length 73;
Best Local Similarity 47.6%; Pred. No. 1.5;
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 3 AHQHSMEIRTPDINPAWYAGR 23
Db 23 AHTHRDEVRSACISVRWLAGR 43

RESULT 8
AH2896
transcription regulator, ROK family Atu2609 [imported] - Agrobacterium tumefaciens (stra
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AH2896
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AH2896
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-308 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL43590.1; PID:g17741107; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu2609
A;Map position: circular chromosome
C;Superfamily: conserved hypothetical protein HI0182; glucose kinase homology

Query Match 30.2%; Score 52; DB 2; Length 308;
Best Local Similarity 50.0%; Pred. No. 6.9;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 3 AHQHSMEIRTPDINPAWYAG 22
Db 196 AHLHRQEMTSEDIIAAWQAG 215

RESULT 9
B97672
rok family protein VC1532 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: B97672
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, P.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: B97672
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-308 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK88331.1; PID:g15157809; GSPDB:GN00169
C;Genetics:
A;Gene: AGR_C_4728
A;Map position: circular chromosome
C;Superfamily: conserved hypothetical protein HI0182; glucose kinase homology

Query Match 30.2%; Score 52; DB 2; Length 308;
Best Local Similarity 50.0%; Pred. No. 6.9;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 3 AHQHSMEIRTPDINPAWYAG 22
Db 196 AHLHRQEMTSEDIIAAWQAG 215

RESULT 10
AH3166
hypothetical protein ugpB [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AH3166
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AH3166
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-419 <KUR>
A;Cross-references: GB:AE008687; PIDN:AAL45750.1; PID:g17743483; GSPDB:GN00188
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: ugpB
A;Genome: plasmid

Query Match 30.2%; Score 52; DB 2; Length 419;
Best Local Similarity 36.8%; Pred. No. 9.6;
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 12 TPDINPAWYAGRGIRPVGR 30
Db 323 SPEANATWFAGTGYLPINK 341

RESULT 11
T31462
probable magnesium chelatase (EC 4.99.1.-) chain H BchH - Heliobacillus mobilis
C;Species: Heliobacillus mobilis
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 15-Sep-2000
C;Accession: T31462
R;Xiong, J.; Inoue, K.; Bauer, C.E.
Proc. Natl. Acad. Sci. U.S.A. 95, 14851-14856, 1998
A;Title: Tracking molecular evolution of photosynthesis by characterization of a majo
A;Reference number: Z21036; MUID:99061957; PMID:9843979
A;Accession: T31462
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1292 <XIO>
A;Cross-references: EMBL:AF080002; NID:g3820536; PID:g3820560; PIDN:AAC84033.1
C;Genetics:
A;Gene: bchH
C;Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase
C;Keywords: lyase

Query Match 30.2%; Score 52; DB 2; Length 1292;
Best Local Similarity 38.5%; Pred. No. 32;
Matches 10; Conservative 3; Mismatches 7; Indels 6; Gaps 1;

Qy 9 EIRTPDINPAWYAG------RGIRPV 28
Db 1176 ETRTKTLNPKWYEGMLKHGYEGVREI 1201

RESULT 12
F83376
conserved hypothetical protein PA2151 [imported] - Pseudomonas aeruginosa (strain PAO
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83376
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; I
.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83376
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-664 <STO>
A;Cross-references: GB:AE004642; GB:AE004091; NID:g9948163; PIDN:AAG05539.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA2151

Query Match 29.9%; Score 51.5; DB 2; Length 664;
Best Local Similarity 55.6%; Pred. No. 19;
Matches 10; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Qy 10 IRTPDINPAWYAGRGIRP 27
: |||||| ': | ||
Db 476 VNTPDINP-WFLQRSGRP 492

RESULT 13
T21075
hypothetical protein F19H6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C;Accession: T21075; T21124
R;McMurray, A.
submitted to the EMBL Data Library, August 1995
A;Reference number: Z19368
A;Accession: T21075
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-294 <WIL>
A;Cross-references: EMBL:Z50873; PIDN:CAA90762.1; GSPDB:GN00028; CESP:F19H6.1
A;Experimental source: clone F17E5
R;McMurray, A.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z19378
A;Accession: T21124
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-294 <WI2>
A;Cross-references: EMBL:Z68115; PIDN:CAA92169.1; GSPDB:GN00028; CESP:F19H6.1
A;Experimental source: clone F19H6
C;Genetics:
A;Gene: CESP:F19H6.1
A;Map position: X
A;Introns: 55/3; 85/2; 113/3; 150/1; 192/3; 266/2
C;Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 29.7%; Score 51; DB 2; Length 294;
Best Local Similarity 44.8%; Pred. No. 9.2;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

Qy 3 AHQHSMEIRTPDINPA--WYAGRGIRPVG 29
|| || | ,| || : | || :|
Db 139 AHMHSKRIMHRDIKPANVFITGNGIVKLG 167

RESULT 14
B69009
conserved hypothetical protein MTH1070 - Methanobacterium thermoautotrophicum (strain De
C;Species: Methanobacterium thermoautotrophicum
C;Date: 29-Jan-1999 #sequence_revision 29-Jan-1999 #text_change 23-Jul-1999
C;Accession: B69009
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: B69009
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-430 <MTH>
A;Cross-references: GB:AE000877; GB:AE000666; NID:g2622157; PIDN:AAB85559.1; PID:g262
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1070
C;Superfamily: conserved hypothetical protein MTH1070

Query Match 29.7%; Score 51; DB 1; Length 430;
Best Local Similarity 69.2%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 14 DINPAWYAGRGIR 26
|||| | ||| |
Db 191 DINPEWVAGRACR 203

RESULT 15
S11210
probable unr protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C;Accession: S11210
R;Jeffers, M.; Paciucci, R.; Pellicer, A.
Nucleic Acids Res. 18, 4891-4899, 1990
A;Title: Characterization of unr; a gene closely linked to N-ras.
A;Reference number: S11210; MUID:90370473; PMID:2204029
A;Accession: S11210
A;Molecule type: mRNA
A;Residues: 1-798 <JEF>
A;Cross-references: EMBL:X52311; NID:g57454; PIDN:CAA36549.1; PID:g57455
C;Keywords: DNA binding

Query Match 29.7%; Score 51; DB 2; Length 798;
Best Local Similarity 43.5%; Pred. No. 27;
Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 6 HSMEIRTPDINPAWYAGRGIRPV 28
|:. | : ;: |:|: ||':
Db 583 HSVNGITEEANPTIYSGKVIRPL 605

Search completed: November 12, 2003, 11:10:05
Job time : 22 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 11:05:42 ; Search time 11 Seconds
(without alignments)
132.530 Million cell updates/sec

Title: US-09-446-543A-5
Perfect score: 172
Sequence: 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	172	100.0	98	1	PRRP_BOVIN	P81264 bos taurus
2	163	94.8	83	1	PRRP_RAT	P81278 rattus norv
3	158	91.9	87	1	PRRP_HUMAN	P81277 homo sapien
4	61	35.5	428	1	NER3_BOVIN	O97859 bos taurus
5	56	32.6	428	1	NER3_HUMAN	Q9uq49 homo sapien
6	52	30.2	417	1	EX7L_CORGL	Q8nrm3 corynebacte
7	52	30.2	447	1	EX7L_COREF	Q8fqp1 corynebacte
8	51	29.7	738	1	UNR_RAT	P18395 rattus norv
9	51	29.7	962	1	UVRA_METTH	O26543 methanobact
10	50	29.1	298	1	Y587_PASMU	Q9cn56 pasteurella
11	50	29.1	973	1	UVRA_RHILO	Q98m36 rhizobium l
12	50	29.1	973	1	UVRA_RHIME	P56899 rhizobium m
13	48.5	28.2	239	1	EPGL_SYNY3	P74618 synechocyst
14	48.5	28.2	1862	1	Y468_MYCPN	P75109 mycoplasma
15	48	27.9	424	1	SAMB_SALTY	P23832 salmonella
16	48	27.9	960	1	UVRA_TREPA	O83527 treponema p
17	47.5	27.6	1083	1	T2D3_HUMAN	O00268 homo sapien
18	47	27.3	406	1	DHI2_RABIT	P51976 oryctolagus
19	47	27.3	418	1	NER3_RAT	Q99pw5 rattus norv
20	47	27.3	442	1	TRB2_METMA	Q8q001 methanosarc
21	47	27.3	940	1	UVRA_VIBCH	Q9kuw5 vibrio chol
22	47	27.3	969	1	UVRA_MYCLE	Q9cc24 mycobacteri
23	47	27.3	972	1	UVRA_MYCTU	P94972 mycobacteri
24	47	27.3	1308	1	M4K6_MOUSE	Q9jm52 mus musculu
25	46.5	27.0	345	1	ARGC_BACHD	Q9k8v2 bacillus ha
26	46.5	27.0	770	1	AVP3_ARATH	P31414 arabidopsis
27	46	26.7	277	1	DAPF_CORGL	Q8np73 corynebacte
28	46	26.7	342	1	Y762_METJA	Q58172 methanococc
29	46	26.7	347	1	Y576_METJA	Q57996 methanococc
30	46	26.7	402	1	EX7L_STRCO	Q9fbm3 streptomyce
31	46	26.7	510	1	YCGB_ECOLI	P29013 escherichia
32	46	26.7	798	1	UNR_HUMAN	O75534 homo sapien
33	46	26.7	836	1	TGM1_RABIT	P22758 oryctolagus
34	46	26.7	943	1	UVRA_HAEIN	P44410 haemophilus
35	46	26.7	943	1	UVRA_PASMU	P57979 pasteurella
36	45.5	26.5	272	1	TRA2_DROVI	O02008 drosophila
37	45.5	26.5	374	1	YHHJ_ECOLI	P31993 escherichia
38	45.5	26.5	411	1	PUR7_ARATH	P38025 arabidopsis
39	45.5	26.5	670	1	SUV1_ARATH	Q9ff80 arabidopsis
40	45.5	26.5	704	1	LIPM_NEIMB	Q05013 neisseria m
41	45	26.2	387	1	HIS8_HALN1	Q9hqs0 halobacteri
42	45	26.2	418	1	NER3_MOUSE	Q9jmh7 mus musculu
43	45	26.2	482	1	R167_YEAST	P39743 saccharomyc
44	45	26.2	676	1	EXL1_HUMAN	Q92935 homo sapien
45	45	26.2	817	1	TGM1_HUMAN	P22735 homo sapien

ALIGNMENTS

RESULT 1
PRRP_BOVIN
ID PRRP_BOVIN STANDARD; PRT; 98 AA.
AC P81264;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing
DE hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-
DE releasing peptide PrRP20].
GN PRH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 23-52.
RC TISSUE=Brain;
RX MEDLINE=98268781; PubMed=9607765;
RA Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S.,
RA Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,
RA Kurokawa T., Nishimura O., Onda H., Fujino M.;
RT "A prolactin-releasing peptide in the brain.";
RL Nature 393:272-276(1998).
CC -!- FUNCTION: Stimulates prolactin (PRL) release and regulates the
CC expression of prolactin through its receptor GPR10. May stimulate
CC lactotrophs directly to secrete PRL.
CC -!- TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
CC ----------
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CC or send an email to license@isb-sib.ch).
CC ----------
DR EMBL; AB015417; BAA29025.1; -.
KW Hormone; Amidation; Signal; Cleavage on pair of basic residues.
FT SIGNAL 1 22
FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP31.
FT PEPTIDE 33 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
FT PROPEP 58 98
FT MOD_RES 53 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
SQ SEQUENCE 98 AA; 10544 MW; 08AC35A13B0FA908 CRC64;

Query Match 100.0%; Score 172; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.8e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
||||||||||||||||||||||||||||||
Db 23 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 53

```
RESULT 2
PRRP_RAT
ID   PRRP_RAT       STANDARD;      PRT;    83 AA.
AC   P81278; Q8K3Y0;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing
DE   hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-
DE   releasing peptide PrRP20].
GN   PRH.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Brain;
RX   MEDLINE=98268781; PubMed=9607765;
RA   Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S.,
RA   Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,
RA   Kurokawa T., Nishimura O., Onda H., Fujino M.;
RT   "A prolactin-releasing peptide in the brain.";
RL   Nature 393:272-276(1998).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   STRAIN=Sprague-Dawley; TISSUE=Hypothalamus;
RA   Anderson S.T., Kokay I.C., Lang T., Grattan D.R., Curlewis J.D.;
RT   "Quantitation of prolactin-releasing peptide (PrRP) mRNA expression in
RT   specific brain regions during the rat oestrous cycle and in
RT   lactation.";
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   TISSUE SPECIFICITY.
RX   MEDLINE=99426652; PubMed=10498338;
RA   Fujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S.,
RA   Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H.,
RA   Sumino Y., Fujino M.;
RT   "Tissue distribution of prolactin-releasing peptide (PrRP) and its
RT   receptor.";
RL   Regul. Pept. 83:1-10(1999).
CC   -!- FUNCTION: Stimulates prolactin (PRL) release and regulates the
CC       expression of prolactin through its receptor GPR10. May stimulate
CC       lactotrophs directly to secrete PRL.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=P81278-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=P81278-2; Sequence=VSP_004370;
CC   -!- TISSUE SPECIFICITY: Widely expressed, with highest levels in
CC       medulla oblongata and hypothalamus.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB015418; BAA29026.1; -.
DR   EMBL; AF521930; AAM82154.1; -.
DR   PIR; JC7607; JC7607.
KW   Hormone; Amidation; Signal; Cleavage on pair of basic residues;
KW   Alternative splicing.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   PEPTIDE      22     52       PROLACTIN-RELEASING PEPTIDE PRRP31.
FT   PEPTIDE      33     52       PROLACTIN-RELEASING PEPTIDE PRRP20.
FT   PROPEP       57     83
FT   MOD_RES      52     52       AMIDATION (G-53 PROVIDE AMIDE GROUP).
FT   VARSPLIC     33     83       TPDINPAWYTGRGIRPVGRFGRRRATPRDVTGLGQLSCLPL
FT                                DGRTKFSQRG -> SECLTYGKQPLTSFHPFTSQMPP (in
FT                                isoform 2).
FT                                /FTId=VSP_004370.
SQ   SEQUENCE   83 AA;  9215 MW;  D0C75A264EEE4F29 CRC64;

  Query Match           94.8%;  Score 163;  DB 1;  Length 83;
  Best Local Similarity  93.5%;  Pred. No. 3.3e-17;
  Matches   29;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              ||||||||| |||||||||| ||||||||||
Db         22 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 52


RESULT 3
PRRP_HUMAN
ID   PRRP_HUMAN     STANDARD;      PRT;    87 AA.
AC   P81277;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing
DE   hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-
DE   releasing peptide PrRP20].
GN   PRH.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=98268781; PubMed=9607765;
RA   Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S.,
RA   Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,
RA   Kurokawa T., Nishimura O., Onda H., Fujino M.;
RT   "A prolactin-releasing peptide in the brain.";
RL   Nature 393:272-276(1998).
RN   [2]
RP   TISSUE SPECIFICITY.
RX   MEDLINE=99426652; PubMed=10498338;
RA   Fujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S.,
RA   Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H.,
RA   Sumino Y., Fujino M.;
RT   "Tissue distribution of prolactin-releasing peptide (PrRP) and its
RT   receptor.";
RL   Regul. Pept. 83:1-10(1999).
CC   -!- FUNCTION: Stimulates prolactin (PRL) release and regulates the
CC       expression of prolactin through its receptor GPR10. May stimulate
CC       lactotrophs directly to secrete PRL.
CC   -!- TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB015419; BAA29027.1; -.
DR   MIM; 602663; -.
DR   GO; GO:0005180; F:peptide hormone; TAS.
KW   Hormone; Amidation; Signal.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   PEPTIDE      23     53       PROLACTIN-RELEASING PEPTIDE PRRP31.
FT   PEPTIDE      34     53       PROLACTIN-RELEASING PEPTIDE PRRP20.
FT   PROPEP       58     87
FT   MOD_RES      53     53       AMIDATION (G-54 PROVIDE AMIDE GROUP).
SQ   SEQUENCE   87 AA;  9639 MW;  229A2F3F50CF981B CRC64;

  Query Match           91.9%;  Score 158;  DB 1;  Length 87;
  Best Local Similarity  90.3%;  Pred. No. 1.9e-16;
  Matches   28;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              |:|||||||||||||||| |||||||||
Db         23 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 53
```

RESULT 4
NER3_BOVIN
ID   NER3_BOVIN   STANDARD;   PRT;   428 AA.
AC   O97859;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Sialidase 3 (EC 3.2.1.18) (Membrane sialidase) (Ganglioside sialidase)
DE   (N-acetyl-alpha-neuraminidase 3).
GN   NEU3.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
RC   TISSUE=Brain;
RX   MEDLINE=99143165; PubMed=9988745;
RA   Miyagi T., Wada T., Iwamatsu A., Hata K., Yoshikawa Y., Tokuyama S.,
RA   Sawada M.;
RT   "Molecular cloning and characterization of a plasma membrane-
RT   associated sialidase specific for gangliosides.";
RL   J. Biol. Chem. 274:5004-5011(1999).
CC   -!- FUNCTION: Plays a role in modulating the ganglioside content of
CC   the lipid bilayer at the level of membrane-bound sialyl
CC   glycoconjugates.
CC   -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC   alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC   oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC   synthetic substrates.
CC   -!- SUBCELLULAR LOCATION: Membrane-associated (By similarity).
CC   -!- TISSUE SPECIFICITY: Expressed in brain.
CC   -!- SIMILARITY: BELONGS TO FAMILY 33 OF GLYCOSYL HYDROLASES.
CC   -!- SIMILARITY: Contains 3 BNR repeats.
CC   ---
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CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; AB008184; BAA75071.1; -.
DR   InterPro; IPR002860; GH_BNR.
DR   Pfam; PF02012; BNR; 3.
KW   Hydrolase; Glycosidase; Membrane; Repeat.
FT   REPEAT   129   140   BNR 1.
FT   REPEAT   203   214   BNR 2.
FT   REPEAT   254   265   BNR 3.
FT   SITE   24   27   FRIP MOTIF.
FT   ACT_SITE   25   25   By similarity.
FT   ACT_SITE   45   45   Potential.
FT   ACT_SITE   50   50   Potential.
FT   ACT_SITE   87   87   Potential.
FT   ACT_SITE   225   225   Potential.
FT   ACT_SITE   245   245   Potential.
FT   ACT_SITE   341   341   By similarity.
FT   ACT_SITE   371   371   Potential.
FT   ACT_SITE   388   388   Potential.
SQ   SEQUENCE   428 AA; 47916 MW; 418B34F3245A8F21 CRC64;

  Query Match   35.5%; Score 61; DB 1; Length 428;
  Best Local Similarity 40.7%; Pred. No. 0.2;
  Matches   11; Conservative   6; Mismatches   10; Indels   0; Gaps   0;

```
Qy          2 RAHQHSMEIRTPDINPAWYAGRGIRPV 28
              ||  ||: | : |:   |: || |:::
Db        195 RARPHSLMIYSDDLGATWHHGRLIKPM 221
```

RESULT 5
NER3_HUMAN
ID   NER3_HUMAN   STANDARD;   PRT;   429 AA.
AC   Q9UQ49; Q9NQE1;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Sialidase 3 (EC 3.2.1.18) (Membrane sialidase) (Ganglioside sialidase)
DE   (N-acetyl-alpha-neuraminidase 3).
GN   NEU3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=99335353; PubMed=10405317;
RA   Wada T., Yoshikawa Y., Tokuyama S., Kuwabara M., Akita H., Miyagi T.;
RT   "Cloning, expression, and chromosomal mapping of a human ganglioside
RT   sialidase.";
RL   Biochem. Biophys. Res. Commun. 261:21-27(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RX   PubMed=10861246;
RA   Monti E., Bassi M.T., Papini N., Riboni M., Manzoni M., Venerando B.,
RA   Croci G., Preti A., Ballabio A., Tettamanti G., Borsani G.;
RT   "Identification and expression of NEU3, a novel human sialidase
RT   associated to the plasma membrane.";
RL   Biochem. J. 349:343-351(2000).
CC   -!- FUNCTION: Plays a role in modulating the ganglioside content of
CC   the lipid bilayer at the level of membrane-bound sialyl
CC   glycoconjugates.
CC   -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC   alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC   oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC   synthetic substrates.
CC   -!- SUBCELLULAR LOCATION: Membrane-associated.
CC   -!- TISSUE SPECIFICITY: Highly expressed in skeletal muscle, testis,
CC   adrenal gland and thymus, followed by pancreas, liver, heart and
CC   thymus. Weakly expressed in kidney, placenta, brain and lung.
CC   -!- MISCELLANEOUS: Optimum pH is 3.8.
CC   -!- SIMILARITY: BELONGS TO FAMILY 33 OF GLYCOSYL HYDROLASES.
CC   -!- SIMILARITY: Contains 3 BNR repeats.
CC   ---
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CC   ---
DR   EMBL; AB008185; BAA82611.1; -.
DR   EMBL; Y18563; CAB96131.1; ALT_INIT.
DR   Genew; HGNC:7760; NEU3.
DR   MIM; 604617; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0006689; P:ganglioside catabolism; TAS.
DR   InterPro; IPR002860; GH_BNR.
DR   Pfam; PF02012; BNR; 3.
KW   Hydrolase; Glycosidase; Membrane; Repeat.
FT   REPEAT   129   140   BNR 1.
FT   REPEAT   203   214   BNR 2.
FT   REPEAT   254   265   BNR 3.
FT   SITE   24   27   FRIP MOTIF.
FT   ACT_SITE   25   25   By similarity.

```
FT   ACT_SITE     45     45       Potential.
FT   ACT_SITE     50     50       Potential.
FT   ACT_SITE     87     87       Potential.
FT   ACT_SITE    225    225       Potential.
FT   ACT_SITE    245    245       Potential.
FT   ACT_SITE    340    340       By similarity.
FT   ACT_SITE    370    370       Potential.
FT   ACT_SITE    387    387       Potential.
SQ   SEQUENCE   428 AA;  48252 MW;  35D1DD9359A78C98 CRC64;

  Query Match             32.6%;  Score 56;  DB 1;  Length 428;
  Best Local Similarity   37.0%;  Pred. No. 1.1;
  Matches   10;  Conservative    6;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          2 RAHQHSMEIRTPDINPAWYAGRGIRPV 28
              :   |:: | : |:   |: :|| |||:
Db        195 KTRPHSLMIYSDDLGVTWHHGRLIRPM 221


RESULT 6
EX7L_CORGL
ID   EX7L_CORGL     STANDARD;      PRT;   417 AA.
AC   Q8NRM3;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
DE   (Exonuclease VII large subunit).
GN   XSEA OR CGL1025.
OS   Corynebacterium glutamicum (Brevibacterium flavum).
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX   NCBI_TaxID=1718;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA   Nakagawa S.;
RT   "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Bidirectionally degrades single-stranded DNA into large
CC       acid-insoluble oligonucleotides, which are then degraded further
CC       into small acid-soluble oligonucleotides (By similarity).
CC   -!- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'-
CC       or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
CC   -!- SUBUNIT: Heterooligomer composed of large and small subunits (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE XSEA FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AP005277; BAB98418.1; -.
DR   HAMAP; MF_00378; -; 1.
DR   InterPro; IPR003753; Exonuc_VII_L.
DR   Pfam; PF02601; Exonuc_VII_L; 1.
DR   TIGRFAMs; TIGR00237; xseA; 1.
KW   Hydrolase; Nuclease; Exonuclease; Complete proteome.
SQ   SEQUENCE   417 AA;  45582 MW;  B32CD9286C173C34 CRC64;

  Query Match             30.2%;  Score 52;  DB 1;  Length 417;
  Best Local Similarity   57.1%;  Pred. No. 4.1;
  Matches   12;  Conservative    1;  Mismatches    0;  Indels    8;  Gaps    1;

Qy         17 PAWYAGRG--------IRPVG 29
              ||:|||||        |||||
Db         94 PAFYAGRGTFSLWVTDIRPVG 114


RESULT 7
EX7L_COREF
ID   EX7L_COREF     STANDARD;      PRT;   447 AA.
AC   Q8FQP1;
DT   15-SEP-2003 (Rel. 42, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
DE   (Exonuclease VII large subunit).
GN   XSEA OR CE1078.
OS   Corynebacterium efficiens.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX   NCBI_TaxID=152794;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA   Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA   Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA   Usuda Y., Sugimoto S.;
RT   "The entire genomic sequence of Corynebacterium efficiens YS-314.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Bidirectionally degrades single-stranded DNA into large
CC       acid-insoluble oligonucleotides, which are then degraded further
CC       into small acid-soluble oligonucleotides (By similarity).
CC   -!- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'-
CC       or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
CC   -!- SUBUNIT: Heterooligomer composed of large and small subunits (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE XSEA FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AP005217; BAC17888.1; -.
DR   HAMAP; MF_00378; -; 1.
DR   InterPro; IPR003753; Exonuc_VII_L.
DR   Pfam; PF02601; Exonuc_VII_L; 1.
DR   TIGRFAMs; TIGR00237; xseA; 1.
KW   Hydrolase; Nuclease; Exonuclease; Complete proteome.
SQ   SEQUENCE   447 AA;  49051 MW;  FDBDF6A768E742C1 CRC64;

  Query Match             30.2%;  Score 52;  DB 1;  Length 447;
  Best Local Similarity   57.1%;  Pred. No. 4.4;
  Matches   12;  Conservative    1;  Mismatches    0;  Indels    8;  Gaps    1;

Qy         17 PAWYAGRG--------IRPVG 29
              ||:|||||        |||||
Db        124 PAFYAGRGSFSLWVTDIRPVG 144


RESULT 8
UNR_RAT
ID   UNR_RAT        STANDARD;      PRT;   798 AA.
AC   P18395;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   UNR protein.
GN   UNR.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RC   TISSUE=Testis;
RX   MEDLINE=90370473; PubMed=2204029;
RA   Jeffers M., Paciucci R., Pellicer A.;
RT   "Characterization of unr; a gene closely linked to N-ras.";
RL   Nucleic Acids Res. 18:4891-4899(1990).
CC   -!- FUNCTION: RNA-BINDING PROTEIN (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X52311; CAA36549.1; -.
DR   PIR; S11210; S11210.
DR   HSSP; P15277; 1MJC.
DR   InterPro; IPR002059; Cold_shock.
DR   Pfam; PF00313; CSD; 7.
DR   ProDom; PD000621; Cold_shock; 1.
DR   SMART; SM00357; CSP; 5.
DR   PROSITE; PS00352; COLD_SHOCK; 4.
KW   RNA-binding; Repeat.
FT   DOMAIN       26     87       CSD 1.
FT   DOMAIN      136    179       CSD 2 (INCOMPLETE).
FT   DOMAIN      186    245       CSD 3.
FT   DOMAIN      297    337       CSD 4 (INCOMPLETE).
FT   DOMAIN      349    410       CSD 5.
FT   DOMAIN      447    507       CSD 6.
FT   DOMAIN      519    579       CSD 7.
FT   DOMAIN      610    670       CSD 8.
FT   DOMAIN      674    735       CSD 9.
SQ   SEQUENCE   798 AA;  88894 MW;  F484B3FA8B0995A4 CRC64;

  Query Match             29.7%;  Score 51;  DB 1;  Length 798;
  Best Local Similarity   43.5%;  Pred. No. 11;
  Matches   10;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          6 HSMEIRTPDINPAWYAGRGIRPV 28
              !|:   | : ||  |:|: |||:
Db        583 HSVNGITEEANPTIYSGKVIRPL 605


RESULT 9
UVRA_METTH
ID   UVRA_METTH     STANDARD;      PRT;   962 AA.
AC   O26543;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A).
GN   UVRA OR MTH443.
OS   Methanobacterium thermoautotrophicum.
OC   Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC   Methanobacteriaceae; Methanothermobacter.
OX   NCBI_TaxID=187420;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Delta H;
RX   MEDLINE=98037514; PubMed=9371463;
RA   Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA   Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA   Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA   Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA   Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA   McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA   Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT   "Complete genome sequence of Methanobacterium thermoautotrophicum
RT   deltaH: functional analysis and comparative genomics.";
RL   J. Bacteriol. 179:7135-7155(1997).
CC   -!- FUNCTION: The UvrABC repair system catalyzes the recognition and
CC       processing of DNA lesions. UvrA is an ATPase and a DNA-binding
CC       protein. A damage recognition complex composed of 2 uvrA and 2
CC       uvrB subunits scans DNA for abnormalities. When the presence of a
CC       lesion has been verified by uvrB, the uvrA molecules dissociate
CC       (By similarity).
CC   -!- SUBUNIT: Forms a heterotetramer with uvrB during the search for
CC       lesions (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. UVRA SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE000828; AAB84949.1; -.
DR   PIR; H69157; H69157.
DR   HAMAP; MF_00205; -; 1.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003439; ABC_transporter.
DR   InterPro; IPR004602; UvrA.
DR   Pfam; PF00005; ABC_tran; 2.
DR   ProDom; PD000006; ABC_transporter; 1.
DR   SMART; SM00382; AAA; 2.
DR   TIGRFAMs; TIGR00630; uvra; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
KW   SOS response; Excision nuclease; DNA repair; DNA recombination;
KW   DNA excision; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
KW   Zinc-finger; Complete proteome.
FT   NP_BIND      38     45       ATP (POTENTIAL).
FT   NP_BIND     649    656       ATP (POTENTIAL).
FT   ZN_FING     748    774       C4-TYPE.
SQ   SEQUENCE   962 AA;  108395 MW;  2C0EF7FC41CCD060 CRC64;

  Query Match             29.7%;  Score 51;  DB 1;  Length 962;
  Best Local Similarity   39.5%;  Pred. No. 14;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels   18;  Gaps    2;

Qy         11 RTPDINPAWYAG----------------RGIRPVGRF 31
              |||  ||| | |                || || |||
Db        703 RTPRSNPATYTGVFTHIRELFAQTPEARKRGYRP-GRF 739


RESULT 10
Y587_PASMU
ID   Y587_PASMU     STANDARD;      PRT;   288 AA.
AC   Q9CN56;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein PM0587.
GN   PM0587.
OS   Pasteurella multocida.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC   Pasteurellaceae; Pasteurella.
OX   NCBI_TaxID=747;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Pm70;
RX   MEDLINE=21145866; PubMed=11248100;
RA   May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT   "Complete genomic sequence of Pasteurella multocida Pm70.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC   -!- SIMILARITY: BELONGS TO THE FRUCTOSAMINE KINASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AE006094; AAK02671.1; -.
DR   InterPro; IPR005581; Fructosamin_kin.
DR   Pfam; PF03881; Fructosamin_kin; 1.
KW   Hypothetical protein; Transferase; Kinase; Complete proteome.
SQ   SEQUENCE   288 AA;  33778 MW;  F4D2F6C26014D940 CRC64;

  Query Match             29.1%;  Score 50;  DB 1;  Length 288;
  Best Local Similarity   37.5%;  Pred. No. 5.4;
  Matches    9;  Conservative    6;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          5 QHSMEIRTPDINPAWYAGRGIRPV 28
              :|  :| | ::: ||    ||:||
Db         20 KHKEKIHTGEMHEAWIIDDGIQPV 43


RESULT 11
UVRA_RHILO
ID   UVRA_RHILO     STANDARD;      PRT;   973 AA.
AC   Q98M36;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A).
GN   UVRA OR MLR0750.
OS   Rhizobium loti (Mesorhizobium loti).
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Phyllobacteriaceae; Mesorhizobium.
OX   NCBI_TaxID=381;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MAFF303099;
RX   MEDLINE=21082930; PubMed=11214968;
RA   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA   Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA   Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA   Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA   Takeuchi C., Yamada M., Tabata S.;
RT   "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT   Mesorhizobium loti.";
RL   DNA Res. 7:331-338(2000).
CC   -!- FUNCTION: The UvrABC repair system catalyzes the recognition and
CC       processing of DNA lesions. UvrA is an ATPase and a DNA-binding
CC       protein. A damage recognition complex composed of 2 uvrA and 2
CC       uvrB subunits scans DNA for abnormalities. When the presence of a
CC       lesion has been verified by uvrB, the uvrA molecules dissociate
CC       (By similarity).
CC   -!- SUBUNIT: Forms a heterotetramer with uvrB during the search for
CC       lesions (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. UVRA SUBFAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AP002995; BAB48277.1; -.
DR   HAMAP; MF_00205; -; 1.
DR   InterPro; IPR003439; ABC_transporter.
DR   InterPro; IPR004602; UvrA.
DR   Pfam; PF00005; ABC_tran; 2.
DR   ProDom; PD000006; ABC_transporter; 1.
DR   TIGRFAMs; TIGR00630; uvra; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW   SOS response; Excision nuclease; DNA repair; DNA recombination;
KW   DNA excision; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
KW   Zinc-finger; Complete proteome.
FT   NP_BIND      34     41       ATP (POTENTIAL).
FT   NP_BIND     662    669       ATP (POTENTIAL).
FT   ZN_FING     761    787       C4-TYPE.
SQ   SEQUENCE   973 AA;  107358 MW;  767D7D2DC8220057 CRC64;

  Query Match             29.1%;  Score 50;  DB 1;  Length 973;
  Best Local Similarity   39.5%;  Pred. No. 19;
  Matches   15;  Conservative    2;  Mismatches    3;  Indels   18;  Gaps    3;

Qy         11 RTPDINPA----------WYAG------RGIRPVGRF 31
              |||  |||          |:||      || :| |||
Db        716 RTPRSNPATYTGAFTPIRDWFAGLPEAKARGYQP-GRF 752


RESULT 12
UVRA_RHIME
ID   UVRA_RHIME     STANDARD;      PRT;   973 AA.
AC   P56899;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A).
GN   UVRA OR R01557 OR SMC01235.
OS   Rhizobium meliloti (Sinorhizobium meliloti).
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
CC   Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX   NCBI_TaxID=382;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1021;
RX   MEDLINE=21396507; PubMed=11481430;
RA   Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA   Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA   Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA   Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA   Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT   "Analysis of the chromosome sequence of the legume symbiont
RT   Sinorhizobium meliloti strain 1021.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
RN   [2]
RP   SEQUENCE OF 1-140 FROM N.A.
RC   STRAIN=2021;
RX   MEDLINE=99430868; PubMed=10503543;
RA   Tapias A., Barbe J.;
RT   "Regulation of divergent transcription from the uvrA-ssb promoters in
RT   Sinorhizobium meliloti.";
RL   Mol. Gen. Genet. 262:121-130(1999).
CC   -!- FUNCTION: The UvrABC repair system catalyzes the recognition and
CC       processing of DNA lesions. UvrA is an ATPase and a DNA-binding
CC       protein. A damage recognition complex composed of 2 uvrA and 2
CC       uvrB subunits scans DNA for abnormalities. When the presence of a
CC       lesion has been verified by uvrB, the uvrA molecules dissociate
CC       (By similarity).
CC   -!- SUBUNIT: Forms a heterotetramer with uvrB during the search for
CC       lesions (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. UVRA SUBFAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AL591787; CAC46136.1; -.
DR   EMBL; AF125162; AAF03210.1; -.
DR   HAMAP; MF_00205; -; 1.
DR   InterPro; IPR003439; ABC_transporter.
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DR   InterPro; IPR004602; UvrA.
DR   Pfam; PF00005; ABC_tran; 2.
DR   ProDom; PD000006; ABC_transporter; 1.
DR   TIGRFAMs; TIGR00630; uvra; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW   SOS response; Excision nuclease; DNA repair; DNA recombination;
KW   DNA excision; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
KW   Zinc-finger; Complete proteome.
FT   NP_BIND      34     41       ATP (POTENTIAL).
FT   NP_BIND     662    669       ATP (POTENTIAL).
FT   ZN_FING     761    787       C4-TYPE.
FT   CONFLICT     19     19       G -> A (IN REF. 2).
FT   CONFLICT     67     67       F -> S (IN REF. 2).
SQ   SEQUENCE   973 AA;  107191 MW;  3E1A8B14527A47FE CRC64;

  Query Match             29.1%;  Score 50;  DB 1;  Length 973;
  Best Local Similarity   39.5%;  Pred. No. 19;
  Matches   15;  Conservative    2;  Mismatches    3;  Indels   18;  Gaps    3;

Qy         11 RTPDINPA----------WYAG------RGIRPVGRF 31
              ||| |||           |:||      || :| |||
Db        716 RTPRSNPATYTGAFTPIRDWFAGLPEAKARGYQP-GRF 752


RESULT 13
6PGL_SYNY3
ID   6PGL_SYNY3     STANDARD;      PRT;   239 AA.
AC   P74618;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   6-phosphogluconolactonase (EC 3.1.1.31) (6PGL).
GN   PGL OR DEVB OR SLL1479.
OS   Synechocystis sp. (strain PCC 6803).
OC   Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX   NCBI_TaxID=1148;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97061201; PubMed=8905231;
RA   Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA   Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
RA   Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA   Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA   Yamada M., Yasuda M., Tabata S.;
RT   "Sequence analysis of the genome of the unicellular cyanobacterium
RT   Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT   entire genome and assignment of potential protein-coding regions.";
RL   DNA Res. 3:109-136(1996).
RN   [2]
RP   SEQUENCE OF 1-19.
RX   MEDLINE=97443974; PubMed=9298645;
RA   Sazuka T., Ohara O.;
RT   "Towards a proteome project of cyanobacterium Synechocystis sp.
RT   strain PCC6803: linking 130 protein spots with their respective
RT   genes.";
RL   Electrophoresis 18:1252-1258(1997).
CC   -!- FUNCTION: HYDROLYSIS OF 6-PHOSPHOGLUCONOLACTONE TO 6-
CC       PHOSPHOGLUCONATE.
CC   -!- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)O = 6-
CC       phospho-D-gluconate.
CC   -!- PATHWAY: Pentose phosphate pathway; second step.
CC   -!- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE
CC       ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D90916; BAA18726.1; ALT_INIT.
DR   InterPro; IPR006148; Gluc_gal_isom.
DR   InterPro; IPR005900; Phosphogluconlac.
DR   Pfam; PF01182; Glucosamine_iso; 1.
DR   TIGRFAMs; TIGR01198; pgl; 1.
KW   Hydrolase; Complete proteome.
FT   INIT_MET      0      0
SQ   SEQUENCE   239 AA;  26351 MW;  9C64A0A342325917 CRC64;

  Query Match             28.2%;  Score 48.5;  DB 1;  Length 239;
  Best Local Similarity   42.3%;  Pred. No. 7.5;
  Matches   11;  Conservative    5;  Mismatches    9;  Indels    1;  Gaps    1;

Qy          5 QHSM-EIRTPDINPAWYAGRGIRPVG 29
              |:: ||  |: :|  |  | |:| |
Db        198 QHALGEIFAPEADPQQYPARFIQPQG 223


RESULT 14
Y468_MYCPN
ID   Y468_MYCPN     STANDARD;      PRT;  1882 AA.
AC   P75109; Q50317;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Protein MG468 homolog (K05_orf1882).
GN   MPN684 OR MP158.
OS   Mycoplasma pneumoniae.
OC   Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=2104;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 29342 / M129;
RX   MEDLINE=97105885; PubMed=8948633;
RA   Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
RA   Herrmann R.;
RT   "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT   pneumoniae.";
RL   Nucleic Acids Res. 24:4420-4449(1996).
RN   [2]
RP   SEQUENCE OF 1-1848 FROM N.A.
RC   STRAIN=ATCC 29342 / M129;
RX   MEDLINE=96177562; PubMed=8604303;
RA   Hilbert H., Himmelreich R., Plagens H., Herrmann R.;
RT   "Sequence analysis of 56 kb from the genome of the bacterium
RT   Mycoplasma pneumoniae comprising the dnaA region, the atp operon and a
RT   cluster of ribosomal protein genes.";
RL   Nucleic Acids Res. 24:628-639(1996).
RN   [3]
RP   IDENTIFICATION BY MASS SPECTROMETRY.
RC   STRAIN=ATCC 29342 / M129;
RX   MEDLINE=21088919; PubMed=11271496;
RA   Regula J.T., Ueberle B., Boguth G., Goerg A., Schnoelzer M.,
RA   Herrmann R., Frank R.;
RT   "Towards a two-dimensional proteome map of Mycoplasma pneumoniae.";
RL   Electrophoresis 21:3765-3780(2000).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: SOME, TO MG064.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AE000017; AAB95806.1; -.
DR   EMBL; U34816; AAC43650.1; -.
DR   PIR; S73484; S73484.
DR   InterPro; IPR003838; DUF214.
DR   Pfam; PF02687; FtsX; 1.
KW   Transmembrane; Complete proteome;
```

```
FT   TRANSMEM     16     36       POTENTIAL.
FT   TRANSMEM    987   1007       POTENTIAL.
FT   TRANSMEM   1037   1057       POTENTIAL.
FT   TRANSMEM   1080   1100       POTENTIAL.
FT   TRANSMEM   1154   1174       POTENTIAL.
FT   TRANSMEM   1759   1779       POTENTIAL.
FT   TRANSMEM   1807   1827       POTENTIAL.
FT   TRANSMEM   1828   1848       POTENTIAL.
FT   TRANSMEM   1851   1871       POTENTIAL.
SQ   SEQUENCE   1882 AA;  209442 MW;  03CFA4D99A7120ED CRC64;

  Query Match             28.2%;  Score 48.5;  DB 1;  Length 1882;
  Best Local Similarity   32.3%;  Pred. No. 64;
  Matches   10;  Conservative    6;  Mismatches   12;  Indels    3;  Gaps    1;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              :|   : : ::.|     |:|   |:|  ||
Db       1188 NRNFNYRLNLQTPTEQSGWYA---IQPYSRF 1215


RESULT 15
SAMB_SALTY
ID   SAMB_SALTY     STANDARD;      PRT;   424 AA.
AC   P23832;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   SamB protein.
GN   SAMB.
OS   Salmonella typhimurium.
OG   Plasmid 60-mDa cryptic.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Salmonella.
OX   NCBI_TaxID=602;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2;
RX   MEDLINE=91123176; PubMed=1991707;
RA   Nohmi T., Hakura A., Nakai Y., Watanabe M., Murayama S.Y.,
RA   Sofuni T.;
RT   "Salmonella typhimurium has two homologous but different umuDC
RT   operons: cloning of a new umuDC-like operon (samAB) present in a
RT   60-megadalton cryptic plasmid of S. typhimurium.";
RL   J. Bacteriol. 173:1051-1063(1991).
CC   -!- FUNCTION: INVOLVED IN UV PROTECTION AND MUTATION.
CC   -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-Y FAMILY.
CC   -!- SIMILARITY: Contains 1 umuC domain.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D90202; BAA14226.1; -.
DR   PIR; B38176; B38176.
DR   HAMAP; MF_01113; atypical; 1.
DR   InterPro; IPR001126; UMUC_like.
DR   Pfam; PF00817; IMS; 1.
DR   PROSITE; PS50173; UMUC; 1.
KW   Plasmid; SOS mutagenesis; DNA repair.
FT   DOMAIN        2    189       UMUC.
SQ   SEQUENCE   424 AA;  47727 MW;  FF8C47476CC58A2B CRC64;

  Query Match             27.9%;  Score 48;  DB 1;  Length 424;
  Best Local Similarity   50.0%;  Pred. No. 16;
  Matches    9;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         10 IRTPDINPAWYAGRGIRP 27
              |  |     |:|||| |
Db        381 INHPGKGKIWFAGRGIAP 398
```

Search completed: November 12, 2003, 11:08:43
Job time : 12 secs

PD 6/23/97

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 12, 2003, 11:06:12 ; Search time 35 Seconds
(without alignments)
228.561 Million cell updates/sec

Title: US-09-446-543A-5
Perfect score: 172
Sequence: 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	172	100.0	98	6	Q8WN12	Q8wn12 ovis aries
2	104	60.5	117	13	Q9W624	Q9w624 carassius a
3	62	36.0	692	2	Q9L8J6	Q9l8j6 rhodospiril
4	57	33.1	54	4	Q9UJF9	Q9ujf9 homo sapien
5	57	33.1	355	5	Q95YJ8	Q95yj8 ciona savig
6	57	33.1	465	4	O60687	O60687 homo sapien
7	57	33.1	465	4	Q8WW85	Q8ww85 homo sapien
8	56.5	32.8	303	16	Q8YWC7	Q8ywc7 anabaena sp
9	55	32.0	1236	2	Q9JPA4	Q9jpa4 rhodocyclus
10	54.5	31.7	503	16	Q9KRY1	Q9kry1 vibrio chol
11	53.5	31.1	176	3	Q08689	Q08689 saccharomyc
12	53	30.8	376	16	Q9RYP2	Q9ryp2 deinococcus
13	53	30.8	467	11	Q8R054	Q8r054 mus musculu
14	53	30.8	468	11	Q8K1F8	Q8k1f8 mus musculu
15	52	30.2	73	16	Q8U515	Q8u515 agrobacteri
16	52	30.2	308	16	Q8UC89	Q8uc89 agrobacteri
17	52	30.2	419	16	Q8UKP2	Q8ukp2 agrobacteri
18	52	30.2	440	11	Q8CBT2	Q8cbt2 mus musculu
19	52	30.2	447	16	Q8FQP1	Q8fqp1 corynebacte
20	52	30.2	848	11	Q8C720	Q8c720 mus musculu
21	52	30.2	1253	2	Q8RTV7	Q8rtv7 uncultured
22	52	30.2	1292	2	Q9ZGE5	Q9zge5 heliobacill
23	52	30.2	3567	11	Q9ES77	Q9es77 mus musculu
24	51.5	29.9	327	10	Q94KU9	Q94ku9 brassica ca
25	51.5	29.9	327	10	Q94FZ9	Q94fz9 brassica ca
26	51.5	29.9	664	16	Q9I1W4	Q9i1w4 pseudomonas
27	51	29.7	184	16	Q8PER0	Q8per0 xanthomonas
28	51	29.7	294	5	Q19530	Q19530 caenorhabdi
29	51	29.7	315	2	O87474	O87474 burkholderi
30	51	29.7	333	4	Q96SD4	Q96sd4 homo sapien
31	51	29.7	367	4	Q8N6Q2	Q8n6q2 homo sapien
32	51	29.7	367	4	Q8IXT2	Q8ixt2 homo sapien
33	51	29.7	370	11	Q8CGW9	Q8cgw9 mus musculu
34	51	29.7	430	17	O27142	O27142 methanobact
35	51	29.7	514	5	Q9VRV3	Q9vrv3 drosophila
36	51	29.7	689	11	Q8R3R1	Q8r3r1 mus musculu
37	51	29.7	767	11	Q8JZN2	Q8jzn2 mus musculu
38	51	29.7	798	11	Q91W50	Q91w50 mus musculu
39	51	29.7	1563	5	Q8T4U2	Q8t4u2 manduca sex
40	51	29.7	1845	17	Q8TTS7	Q8tts7 methanosarc
41	50.5	29.4	292	10	Q8S7E3	Q8s7e3 oryza sativ
42	50.5	29.4	374	16	Q8ZLE1	Q8zle1 salmonella
43	50.5	29.4	420	2	Q93LZ7	Q93lz7 streptomyce
44	50.5	29.4	790	10	Q9M371	Q9m371 arabidopsis
45	50	29.1	217	16	Q8PQ42	Q8pq42 xanthomonas

ALIGNMENTS

RESULT 1
Q8WN12
ID Q8WN12 PRELIMINARY; PRT; 98 AA.
AC Q8WN12;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Preproprolactin-releasing peptide.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Curlewis J.D., Kusters D.H.L., Barclay J.L., Anderson S.T.;
RT "Prolactin-releasing peptide (PrRP) in the ewe: cDNA cloning, mRNA
RT distribution and effects on prolactin secretion in vitro and in
RT vivo.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF450453; AAL47178.1; -.
SQ SEQUENCE 98 AA; 10513 MW; 2A53331ED62CAAB5 CRC64;

Query Match 100.0%; Score 172; DB 6; Length 98;
Best Local Similarity 100.0%; Pred. No. 9.2e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
Db 23 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 53

RESULT 2
Q9W624
ID Q9W624 PRELIMINARY; PRT; 117 AA.
AC Q9W624;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

```
DE   C-RF amide.
OS   Carassius auratus (Goldfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Carassius.
OX   NCBI_TaxID=7957;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Satake H., Minakata H., Fujimoto M.;
RT   "Carassius RFamide (C-RF amide).";
RL   Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB020024; BAA76662.1; -.
SQ   SEQUENCE   117 AA;  12879 MW;  D5DC4CB22038C2B0 CRC64;

  Query Match             60.5%;  Score 104;  DB 13;  Length 117;
  Best Local Similarity   57.7%;  Pred. No. 4.8e-07;
  Matches   15;  Conservative    8;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 HSMEIRTPDINPAWYAGRGIRPVGRF 31
              |::: |:|:|:| || |||:||::||
Db         50 HNVDNRSPEIDPFWYVGRGVRPIGRF 75


RESULT 3
Q9L8J6
ID   Q9L8J6      PRELIMINARY;      PRT;   692 AA.
AC   Q9L8J6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   BchH (Fragment).
GN   BCHH.
OS   Rhodospirillum rubrum.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC   Rhodospirillaceae; Rhodospirillum.
OX   NCBI_TaxID=1085;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=R5;
RX   MEDLINE=20138142; PubMed=10671438;
RA   Cheng Y.S., Brantner C.A., Tsapin A., Collins M.L.P.;
RT   "Role of the H protein in assembly of the photochemical reaction
RT   center and intracytoplasmic membrane in Rhodospirillum rubrum.";
RL   J. Bacteriol. 182:1200-1207(2000).
DR   EMBL; AF202319; AAF37352.1; -.
DR   InterPro; IPR003672; CobN/Mg_chltase.
DR   Pfam; PF02514; cobN-Mg_chel; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   692 AA;  75453 MW;  96430AE93BF35680 CRC64;

  Query Match             36.0%;  Score 62;  DB 2;  Length 692;
  Best Local Similarity   40.6%;  Pred. No. 2.7;
  Matches   13;  Conservative    4;  Mismatches    9;  Indels    6;  Gaps    1;

Qy          3 AHQHSMEIRTPDINPAWYAG------RGIRPV 28
              | | |:| ||  :|| || |       |:| :
Db        568 AEQVSLETRTRALNPKWYEGMLAHGYEGVRQI 599


RESULT 4
Q9UJF9
ID   Q9UJF9      PRELIMINARY;      PRT;    54 AA.
AC   Q9UJF9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   DJ479J7.3 (Sushi-repeat protein (SRPUL)) (Fragment).
GN   DJ479J7.3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lawlor S.;
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL035608; CAB55682.1; -.
FT   NON_TER      54     54
SQ   SEQUENCE   54 AA;  6110 MW;  E2F3C39F7B961A9F CRC64;

  Query Match             33.1%;  Score 57;  DB 4;  Length 54;
  Best Local Similarity   56.2%;  Pred. No. 0.98;
  Matches    9;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         12 TPDINPAWYAGRGIRP 27
              |: : | |||| |  |
Db         18 TPAVTPTWYAGSGYYP 33


RESULT 5
Q95YJ8
ID   Q95YJ8      PRELIMINARY;      PRT;   355 AA.
AC   Q95YJ8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Zic related protein 1a.
GN   CS-ZICR1A.
OS   Ciona savignyi.
OC   Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC   Phlebobranchia; Cionidae; Ciona.
OX   NCBI_TaxID=51511;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Imai K.S., Satoh N., Satou Y.;
RT   "Ciona savignyi genes.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB057747; BAB68356.1; -.
DR   InterPro; IPR007087; Znf_C2H2.
DR   Pfam; PF00096; zf-C2H2; 4.
DR   SMART; SM00355; ZnF_C2H2; 4.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
KW   Metal-binding; Zinc; Zinc-finger.
SQ   SEQUENCE   355 AA;  40876 MW;  E58F5DEDD812E8AC CRC64;

  Query Match             33.1%;  Score 57;  DB 5;  Length 355;
  Best Local Similarity   40.0%;  Pred. No. 7;
  Matches   12;  Conservative    7;  Mismatches    7;  Indels    4;  Gaps    1;

Qy          2 RAHQHSMEIRTPDIN----PAWYAGRGIRP 27
              :|||:|:: :   :|     |:||| |: |
Db         27 QAHQHSIDSKPMQLNSVPSAAYYAGYGMIP 56


RESULT 6
O60687
ID   O60687      PRELIMINARY;      PRT;   465 AA.
AC   O60687;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Sushi-repeat protein (Sushi-repeat containing protein).
GN   SRPUL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kurosawa H., Inukai T., Inaba T., Goi K., Chang K.-S., Sinjyo T.,
RA   Rakestraw K.M., Naeve C.W., Look T.A.;
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
```

```
RA   Huang C.-H., Chen H., Peng J., Chen Y.;
RT   "Cloning and characterization of the sushi-repeat containing protein
RT   (SRP) as a novel interaction partner of Rh type C glycoprotein
RT   (RhCG).";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF060567; AAC15765.1; -.
DR   EMBL; AF393649; AAM73693.1; -.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   InterPro; IPR003410; Hyalin.
DR   InterPro; IPR000436; Sushi_SCR_CCP.
DR   Pfam; PF02494; HYR; 1.
DR   Pfam; PF00084; sushi; 3.
DR   PROSITE; PS00086; CYTOCHROME_P450; 1.
SQ   SEQUENCE   465 AA;  52971 MW;  4D752B187FF3EFB8 CRC64;

  Query Match             33.1%;  Score 57;  DB 4;  Length 465;
  Best Local Similarity   56.2%;  Pred. No. 9.2;
  Matches    9;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         12 TPDINPAWYAGRGIRP 27
              || : | |:|: | | |
Db         18 TPAVTPTWYAGSGYYP 33


RESULT 7
Q8WW85
ID   Q8WW85      PRELIMINARY;      PRT;   465 AA.
AC   Q8WW85;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Sushi-repeat protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RA   Strausberg R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC020733; AAH20733.1; -.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   InterPro; IPR003410; Hyalin.
DR   InterPro; IPR000436; Sushi_SCR_CCP.
DR   Pfam; PF02494; HYR; 1.
DR   Pfam; PF00084; sushi; 3.
DR   SMART; SM00032; CCP; 3.
DR   PROSITE; PS00086; CYTOCHROME_P450; 1.
SQ   SEQUENCE   465 AA;  52957 MW;  3D7229487DA1B8BD CRC64;

  Query Match             33.1%;  Score 57;  DB 4;  Length 465;
  Best Local Similarity   56.2%;  Pred. No. 9.2;
  Matches    9;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         12 TPDINPAWYAGRGIRP 27
              || : | ||||  |  |
Db         18 TPAVTPTWYAGSGYYP 33


RESULT 8
Q8YWC7
ID   Q8YWC7      PRELIMINARY;      PRT;   303 AA.
AC   Q8YWC7;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein All1686.
GN   All1686.
OS   Anabaena sp. (strain PCC 7120).
OC   Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX   NCBI_TaxID=103690;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21595285; PubMed=11759840;
RA   Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA   Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA   Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA   Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA   Yasuda M., Tabata S.;
RT   "Complete genomic sequence of the filamentous nitrogen-fixing
RT   cyanobacterium Anabaena sp. strain PCC 7120.";
RL   DNA Res. 8:205-213(2001).
DR   EMBL; AP003586; BAB78052.1; -.
DR   InterPro; IPR004843; M-ppestrase.
DR   Pfam; PF00149; Metallophos; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   303 AA;  34449 MW;  685700B2127EE987 CRC64;

  Query Match             32.8%;  Score 56.5;  DB 16;  Length 303;
  Best Local Similarity   51.6%;  Pred. No. 7;
  Matches   16;  Conservative    2;  Mismatches    8;  Indels    5;  Gaps    2;

Qy          4 HQHSMEIRTPDINPAWY----AGRGIRPVGR 30
              |:|| | ||  .:   |    || | ||||
Db        226 HEHSYE-RTRAIDGTTYLTCGAGAGNRPVGR 255


RESULT 9
Q9JPA4
ID   Q9JPA4      PRELIMINARY;      PRT;  1236 AA.
AC   Q9JPA4;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Mg protoporphyrin methyl transferase.
GN   BCHH.
OS   Rhodocyclus gelatinosus (Rhodopseudomonas gelatinosa).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Comamonadaceae; Rubrivivax.
OX   NCBI_TaxID=28068;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IL144;
RA   Nagashima K.V., Shimada K., Matsuura K.;
RT   "Phylogenetic analysis of photosynthetic genes of Rhodocyclus
RT   gelatinosus: Possibility of horizontal gene transfer in purple
RT   bacteria.";
RL   Photosyn. Res. 36:185-191(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IL144;
RX   MEDLINE=94132007; PubMed=8300574;
RA   Nagashima K.V., Matsuura K., Ohyama S., Shimada K.;
RT   "Primary structure and transcription of genes encoding B870 and
RT   photosynthetic reaction center apoproteins from Rubrivivax
RT   gelatinosus.";
RL   J. Biol. Chem. 269:2477-2484(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IL144;
RA   Igarashi N., Shimada K., Matsuura K., Nagashima K.V.;
RT   "Photosynthetic gene cluster in purple bacterium, Rubrivivax
RT   gelatinosus.";
RL   (In) Garab G. (eds.);
RL   Photosynthesis:
RL   mechanisms and effects (Proceedings of the 11th international congress
RL   on photosynthesis), pp.4:2889-2892, Kluwer Academic Publishers,
RL   Dordrecht (1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IL144;
RX   MEDLINE=20031519; PubMed=10563807;
RA   Menin L., Yoshida M., Jaquinod M., Nagashima K.V., Matsuura K.,
RA   Parot P., Vermeglio A.;
RT   "Dark aerobic growth conditions induce the synthesis of a high
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RT   midpoint potential cytochrome c8 in the photosynthetic bacterium
RT   Rubrivivax gelatinosus.";
RL   Biochemistry 38:15238-15244(1999).
DR   EMBL; AB034704; BAA94057.1; -.
DR   InterPro; IPR003672; CobN/Mg_chltase.
DR   Pfam; PF02514; cobN-Mg_chel; 1.
KW   Transferase.
SQ   SEQUENCE   1236 AA;  134729 MW;  84051C045638520C CRC64;

  Query Match             32.0%;  Score 55;  DB 2;  Length 1236;
  Best Local Similarity   34.4%;  Pred. No. 49;
  Matches   11;  Conservative    6;  Mismatches    9;  Indels    6;  Gaps    1;

Qy          3 AHQHSMEIRTPDINPAWYAG------RGIRPV 28
              : | ::| || :|| || |       |:| :
Db       1112 SEQVALETRTRMLNPKWYEGMLEHGYEGVRQI 1143


RESULT 10
Q9KRY1
ID   Q9KRY1      PRELIMINARY;      PRT;   503 AA.
AC   Q9KRY1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Sun/nucleolar protein family protein.
GN   VC1502.
OS   Vibrio cholerae.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC   Vibrionaceae; Vibrio.
OX   NCBI_TaxID=666;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=El Tor N16961 / Serotype O1;
RX   MEDLINE=20406833; PubMed=10952301;
RA   Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA   Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA   Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA   Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA   McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA   Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA   Fraser C.M.;
RT   "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT   cholerae.";
RL   Nature 406:477-483(2000).
DR   EMBL; AE004228; AAF94657.1; -.
DR   TIGR; VC1502; -.
DR   InterPro; IPR000051; SAM_bind.
DR   InterPro; IPR001678; Sun_Nop1/Nop2.
DR   Pfam; PF01189; Nol1_Nop2_Sun; 1.
DR   TIGRFAMs; TIGR00446; nop2p; 1.
DR   PROSITE; PS01153; NOL1_NOP2_SUN; 1.
KW   Complete proteome.
SQ   SEQUENCE   503 AA;  55997 MW;  2ABD94A2356C9E48 CRC64;

  Query Match             31.7%;  Score 54.5;  DB 16;  Length 503;
  Best Local Similarity   36.7%;  Pred. No. 23;
  Matches   11;  Conservative    6;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
                :  ||:|: |      |: || :|| |:
Db        435 SSSASHSVELDTTQAR-EWFMGRDVRPEGQ 463


RESULT 11
Q08689
ID   Q08689      PRELIMINARY;      PRT;   176 AA.
AC   Q08689;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Chromosome XV reading frame ORF YOR253W.
GN   ARD2 OR YOR253W.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   MIPS;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97298311; PubMed=9153759;
RA   Jauniaux J.C., Poirey R.;
RT   "Sequencing analysis of a 36.9 kb fragment of yeast chromosome XV
RT   reveals 26 open reading frames including SEC63, CDC31, SUG2, GCD1,
RT   RBL2, PNT1, PAC1 and VPH1.";
RL   Yeast 13:483-487(1997).
DR   EMBL; Z75161; CAA99475.1; -.
DR   SGD; S0005779; ARD2.
DR   InterPro; IPR000345; CytC_heme_bind.
DR   InterPro; IPR000182; GCN5acetyltransf.
DR   Pfam; PF00583; Acetyltransf; 1.
DR   PROSITE; PS00190; CYTOCHROME_C; 1.
SQ   SEQUENCE   176 AA;  19727 MW;  4F09DC597A690BA0 CRC64;

  Query Match             31.1%;  Score 53.5;  DB 3;  Length 176;
  Best Local Similarity   31.2%;  Pred. No. 11;
  Matches   10;  Conservative    5;  Mismatches   14;  Indels    3;  Gaps    1;

Qy          1 SRAHQHSMEIRTP---DINPAWYAGRGIRPVG 29
                |  |||:: :  |   |:   |: | |   ||
Db        120 SECHQHNVFVYLPAVDDLTKQWFIAHGFEQVG 151


RESULT 12
Q9RYP2
ID   Q9RYP2      PRELIMINARY;      PRT;   376 AA.
AC   Q9RYP2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Adenine deaminase-related protein.
GN   DRA0268.
OS   Deinococcus radiodurans.
OC   Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC   Deinococcaceae; Deinococcus.
OX   NCBI_TaxID=1299;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=R1;
RX   MEDLINE=20036896; PubMed=10567266;
RA   White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA   Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA   Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA   Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA   Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA   Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA   Fraser C.M.;
RT   "Genome sequence of the radioresistant bacterium Deinococcus
RT   radiodurans R1.";
RL   Science 286:1571-1577(1999).
DR   EMBL; AE001863; AAF12376.1; -.
DR   TIGR; DRA0268; -.
KW   Complete proteome.
SQ   SEQUENCE   376 AA;  39845 MW;  7AB7FF32F8C45651 CRC64;

  Query Match             30.8%;  Score 53;  DB 16;  Length 376;
  Best Local Similarity   40.0%;  Pred. No. 27;
  Matches   12;  Conservative    6;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
              :||  |: ::  || : |  ||:  || ||
Db        177 ARALAHAPDVSRPDRHRACGAGQRRRPAGR 206
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RESULT 13
Q8R054
ID   Q8R054      PRELIMINARY;      PRT;   467 AA.
AC   Q8R054;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Similar to sushi-repeat protein.
GN   1110039C07RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC028307; AAH28307.1; -.
DR   MGD; MGI:1916042; 1110039C07Rik.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   InterPro; IPR003410; Hyalin.
DR   InterPro; IPR000436; Sushi_SCR_CCP.
DR   Pfam; PF02494; HYR; 1.
DR   Pfam; PF00084; sushi; 3.
DR   SMART; SM00032; CCP; 3.
DR   PROSITE; PS00086; CYTOCHROME_P450; 1.
SQ   SEQUENCE   467 AA;  53009 MW;  BB4C01C7E6118BE0 CRC64;

  Query Match             30.8%;  Score 53;  DB 11;  Length 467;
  Best Local Similarity   53.3%;  Pred. No. 34;
  Matches    8;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         13 PDINPAWYAGRGIRP 27
              | : | ||| | | :
Db         19 PAVTPTWYAGSGYSP 33


RESULT 14
Q8K1F8
ID   Q8K1F8      PRELIMINARY;      PRT;   468 AA.
AC   Q8K1F8;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Sushi-repeat containing protein.
GN   1110039C07RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Huang C.-H., Chen H., Peng J., Chen Y.;
RT   "Cloning and characterization of the sushi-repeat containing protein
RT   (SRP) as a novel interaction partner of Rh type C glycoprotein
RT   (RhCG).";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF393640; AAM73691.1; -.
DR   MGD; MGI:1916042; 1110039C07Rik.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   InterPro; IPR003410; Hyalin.
DR   InterPro; IPR000436; Sushi_SCR_CCP.
DR   Pfam; PF02494; HYR; 1.
DR   Pfam; PF00084; sushi; 3.
DR   SMART; SM00032; CCP; 3.
DR   PROSITE; PS00086; CYTOCHROME_P450; 1.
SQ   SEQUENCE   468 AA;  53180 MW;  151A952070D040D4 CRC64;

  Query Match             30.8%;  Score 53;  DB 11;  Length 468;
  Best Local Similarity   53.3%;  Pred. No. 34;
  Matches    8;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         13 PDINPAWYAGRGIRP 27
              | : | ||| | | :
Db         20 PAVTPTWYAGSGYSP 34


RESULT 15
Q8U515
ID   Q8U515      PRELIMINARY;      PRT;    73 AA.
AC   Q8U515;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   AGR_L_109p.
GN   AGR_L_109.
OS   Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Rhizobiaceae; Rhizobium.
OX   NCBI_TaxID=176299;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21608551; PubMed=11743194;
RA   Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA   Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA   Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA   Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA   Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA   Cielo C., Slater S.;
RT   "Genome sequence of the plant pathogen and biotechnology agent
RT   Agrobacterium tumefaciens C58.";
RL   Science 294:2323-2328(2001).
DR   EMBL; AE008203; AAK88619.1; -.
SQ   SEQUENCE   73 AA;  8219 MW;  02A6F70FA651F2AB CRC64;

  Query Match             30.2%;  Score 52;  DB 16;  Length 73;
  Best Local Similarity   47.6%;  Pred. No. 6.9;
  Matches   10;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 AHQHSMEIRTPDINPAWYAGR 23
              :| |  |:|:  |:  | |||
Db         23 AHTHRDEVRSACISVRWLAGR 43


Search completed: November 12, 2003, 11:09:32
Job time : 37 secs
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